

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
Run on: December 28, 2000, 09:56:08 ; Search time 2435.54 Seconds
(without alignments)
3929.054 Million cell updates/sec

Title: US-08-989-362-1
Perfect score: 2191
Sequence: 1 GCCAGGACCTCTGTCAACCG.....TTTTGGTACTTAAAAATGCC 2191

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues 2067340
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
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2: gb_ba2.*
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4: gb_ov.*
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6: gb_ph.*
7: gb_pl1.*
8: gb_pl2.*
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10: gb_pr2.*
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88: gb_htg21.*
89: gb_htg22.*
90: gb_htg23.*
91: gb_sts1.*
92: gb_sts2.*
93: gb_v11.*
94: gb_v12.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2144.8	97.9	2295	5	AR062119	AR062119 Sequence
2	2144.8	97.9	2299	12	AF053713	AF053713 Mus muscu
3	2143.2	97.8	2225	12	AF019048	AF019048 Mus muscu
4	2049.2	93.5	2237	12	AF013170	AF013170 Mus muscu
5	1460.8	66.7	2029	12	AB022036S4	AB022039 Mus muscu
6	1118.8	51.1	2271	11	AF053712	AF053712 Homo sapi
7	1107.8	50.6	2201	11	AF019047	AF019047 Homo sapi
8	957.2	43.7	1823	11	AF013171	AF013171 Homo sapi
9	951	43.4	951	12	AB008426	AB008426 Mus muscu
10	951	43.4	951	12	AB036798	AB036798 Mus muscu
11	818.2	37.3	864	12	AB032771	AB032771 Mus muscu
12	771.8	35.2	205139	85	AL139382	AL139382 Homo sapi

13	726	33.1	754	12	AB03:1772	Mus muscu
14	688.4	31.4	113451	77	AC02:1297	AB03:2772 Homo sapi
15	545.8	24.9	930	79	AB03:1999	AB03:7599 Homo sapi
16	347.4	15.9	764	12	AB02:2036S1	AB02:2036 Mus muscu
17	167.4	7.6	468	12	AB02:2036S2	AB02:2037 Mus muscu
18	105.8	4.8	575	15	AB02:2036S3	AB02:2038 Mus muscu
19	97	4.4	194030	70	AC01:1969	AB01:0969 Homo sapi
20	74.2	3.4	4362	33	DDU60170	U60170 Dictyostell
21	72.2	3.3	113451	77	AC02:1297	AC02:3297 Homo sapi
22	72	3.3	150754	11	AC02:1491	AC02:3491 Homo sapi
23	72	3.3	175358	10	AC00:1981	AC00:7981 Homo sapi
24	64.8	3.0	1100000	90	PFMA:13P2_2	Continuation (3 of
25	64.2	2.9	94384	11	AC01:1718	AC01:1718 Homo sapi
26	64	2.9	12900	31	AE00:1429	AE00:1429 Plasmodiu
27	63.4	2.9	256172	68	AC00:1319	AC00:5139 Plasmodiu
28	63.2	2.9	13859	31	AE00:1366	AE00:1366 Plasmodiu
29	62	2.8	63282	75	AC02:1756	AC02:0756 Homo sapi
30	62	2.8	160401	69	AC02:1077	AC00:9277 Homo sapi
31	61.2	2.8	182340	75	AC02:1206	AC02:1006 Homo sapi
32	60.8	2.8	1181	34	MSC:X13	X14910 Yeast mitoc
33	60.8	2.8	85779	34	SC00:11856	AC01:1856 Saccharom
34	60.8	2.8	158250	75	AC02:3781	AC02:0781 Homo sapi
35	60.6	2.8	151922	68	AC00:3278	AC00:6278 Plasmodiu
36	60.4	2.8	176552	9	AC00:4317	AC00:4617 Homo sapi
37	60	2.7	151941	73	AC01:5938	AC01:15938 Homo sapi
38	60	2.7	167810	10	AC00:7051	AC00:7051 Homo sapi
39	59.8	2.7	13684	31	AE00:1403	AE00:1403 Plasmodiu
40	59.8	2.7	234112	33	PFMA:4P2	AL035475 Plasmodiu
41	59.6	2.7	2858	34	YSCMTCG38	L36902 Saccharomyc
42	59.6	2.7	12813	33	AE00:1382	AE00:1382 Plasmodiu
43	59.6	2.7	66441	33	PFMAL1P4	AL031747 Plasmodiu
44	59.2	2.7	14867	31	AE00:1398	AE00:1398 Plasmodiu
45	59.2	2.7	157016	70	AC01:0948	AC01:0948 Homo sapi

Db	154	CGCCATTCGCGCGCGCCACCGCAGACTACGGCAAGTACTTCGCGAGCTTCGGAGGAGATGGG	213
QY	181	CACGGCGCCGCGCTCCACACGAGGGTCGCTGCACCCCGCGCTTCTGCACCGCGCTCC	240
Db	214	CACGGCGCCGCGCTCCACACGAGGGTCGCTGCACCCCGCGCTTCTGCACCGCGCTCC	273
QY	241	GGCGCGCCACCGCGCGCTCCCGCTCCATGTTCCTTCGGCCCTCCTGGGGTGGGACATGGG	300
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QY	301	CCAGGTGGTCTGCAGCATCGCTCTGTTCCTGTACTTTCGAGCGCAGATGGATCCTTAACAG	360
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QY	361	AATATCAGAGACAGCACTCACTTCCTTTTATAGAACTCTGAGACTCCTGAAACGCGAGG	420
Db	394	AATATCAGAGACAGCACTCACTTCCTTTTATAGAACTCTGAGACTCCTGAAACGCGAGG	453
QY	421	TTTTCGAGGACTCGACTCTTGAGAGTGAAGACACACTACCTGACTCCTTCGAGGAGGATGAA	480
Db	454	TTTTCGAGGACTCGACTCTTGAGAGTGNAGACACACTACCTGACTCCTTCGAGGAGGATGAA	513
QY	481	ACAAGCCTTTCAGGGGGCGTGCAGAGGAACATGCAACACATTTGTGGGGCCACACGCTT	540
Db	514	ACAAGCCTTTCAGGGGGCGTGCAGAGGAACATGCAACACATTTGTGGGGCCACACGCTT	573
QY	541	CTCAGGAGTCCAGCTATGATGAGAGGCTCATGGTTGGATGTGGCCACGCGGCAAGCC	600
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QY	601	TGAGGGCCACGCCATTTTCACACCTTCACCATCAATGCTGCCAGCATCCATCGGGTTCCCA	660
Db	634	TGAGGGCCACGCCATTTTCACACCTTCACCATCAATGCTGCCAGCATCCATCGGGTTCCCA	693
QY	661	TAAAGTCACTCTCTCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAACATGAC	720
Db	694	TAAAGTCACTCTCTCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAACATGAC	753
QY	721	GTTAAGCAACGGAAACTRAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCACAT	780
Db	754	GTTAAGCAACGGAAACTRAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCACAT	813
QY	781	TTGCTTTTCGGCATCATGAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGT	840
Db	814	TTGCTTTTCGGCATCATGAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGT	873
QY	841	GTATGTGTTAAACACAGCATCAAAATCCCAAGTCTCATACCTGATGAAGAGGGAG	900
Db	874	GTATGTGTTAAACACAGCATCAAAATCCCAAGTCTCATACCTGATGAAGAGGGAG	933
QY	901	CAGGAAAACTGGTCGGCAATTCTGAATTCACATTTTATTCATTAATCTTGGGGATT	960
Db	934	CAGGAAAACTGGTCGGCAATTCTGAATTCACATTTTATTCATTAATCTTGGGGATT	993
QY	961	TTTCAAGCTCCGAGCTGGTGAAGAAATTAGCATTCAGGTTCCAACCTTCCCTGCTGGA	1020
Db	994	TTTCAAGCTCCGAGCTGGTGAAGAAATTAGCATTCAGGTTCCAACCTTCCCTGCTGGA	1053
QY	1021	TCCGGATCAAGATGCGACGTACTTTGGGGCTTTCAAGATTTCAGACATAGACTGAGACT	1080
Db	1054	TCCGGATCAAGATGCGACGTACTTTGGGGCTTTCAAGATTTCAGACATAGACTGAGACT	1113
QY	1081	ATTTCGTGGACATTAGCATGGATGTCTAGATGTTTGGAAACTTCTTAAAAATGGATG	1140
Db	1114	ATTTCGTGGACATTAGCATGGATGTCTAGATGTTTGGAAACTTCTTAAAAATGGATG	1173
QY	1141	ATGCTCTATACATGTGTAAGACTACTAAGACACATGGCCCAAGTGTATGAACTTCACAGC	1200
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QY	1201	CCTCTCTCTTGACCTGTACAGGTTGTGTATATGTAAAGTCCATAGGTGATGTAGATTC	1260
Db	1234	CCTCTCTCTTGACCTGTACAGGTTGTGTATATGTAAAGTCCATAGGTGATGTAGATTC	1293

ALIGNMENTS									
RESULT 1									
AR062119	2295 bp	DNA							
SEQUENCE	6 from patent	US 5843678							
AR062119									
AR062119.1	GI:5989810								
UNKNOWN									
UNCLASSIFIED									
1 (bases 1 to 2295)									
Boyle, W.J.									
Osteoprotegerin binding proteins									
Patent: US 5843678-A 6 01-DEC-1998;									
Location/Qualifiers									
1..2295									
/organism="unknown"									
648 a	487 c	538 g	622 t						
QUERY MATCH									
Query Match	97.9%	Score 2144.8;	DB 5;	Length 2295;					
Best Local Similarity	99.4%	Pos. No. 0;							
Matches 2174;	Conservative	0;	Mismatches	12;	Indels	2;	Gaps		
1	GCACGAGCTCTGTGAACCGGTTCGGGK	GGGGCGCCCTGGCCGGAGTCTGCTCGGCGG	60						
34	GCACGAGCTCTGTGAACCGGTTCGGGK	GGGGCGCCCTGGCCGGAGTCTGCTCGGCGG	93						
61	TGGGTGGCCGAGGAGAGGAGAACGAT	CGCGAGCAGGCGCCCGAACTCGGGCGCGG	120						
94	TGGGTGGCCGAGGAGAGGAGAACGAT	CGCGAGCAGGCGCCCGAACTCGGGCGCGG	153						
121	CGCCATGGCCCGGCGCAGCCGAGACTA	GGCAAGTACCTGGCCGAGCTCGGAGGATGGG	180						

Db 466 TTTTGCAGGACTCGACTCTGAGAGTGAAGACACACTACCTGACTCTCTGCAGGAGGATGAA 525
QY 481 ACAAGCCCTTCAGGGGCCGTGCAGAAAGAACTGCAACACATATGTGGGGCCACAGCGCTT 540
Db 526 ACAAGCCCTTCAGGGGCCGTGCAGAAAGAACTGCAACACATATGTGGGGCCACAGCGCTT 585
QY 541 CTGAGGAGCTCCAGCTATGATGAGAGCCATCATGCTTGGATGTGGCCCGCAGGAGCAAGCC 600
Db 586 CTGAGGAGCTCCAGCTATGATGAGAGCCATCATGCTTGGATGTGGCCCGCAGGAGCAAGCC 645
QY 601 TGAGGGCCAGCCATTTTCACACACCTCACATCAATGCTGCCAGCATCCCATCGGGTCCCA 660
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QY 661 TAAAGTCACTCTGTCTCTTGGTACCACTATCGAGGGCTGGGCCAAGATCTCTAACATGAC 720
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QY 721 GTTAAAGCAAGCAAACTAAGGGTTAACTAAGATGGCTTCTATTAACCTGTACGCCCAACAT 780
Db 766 GTTAAAGCAAGCAAACTAAGGGTTAACTAAGATGGCTTCTATTAACCTGTACGCCCAACAT 825
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P. 11

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Db 1965 GCTAATGCACTTTAGGAGCTGACATAGCAAAAGGATACATAATAGCTACTGAAAAATC 2023
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Db 2024 TGTCAGGAGTATTTATGCAATTTATGAACAGGTGTCTTTTTCACAGAGCTTACAAATG 2083
QY 2041 TAAATTTGTTCTTTTTCCTCCATAGAAATGTACTATAGTTATCAGCCCAAAACA 2100
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QY 2101 ATCCACTTTTTTAATTTAGTGAAGTTATTTATTTACTGTACATAAAGCATTTGTTTC 2160
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QY 2161 TGAATGGCATTTTTCGTTACTTAAATAT 2188
Db 2204 TGAATGTTAATTTTTCGTTACTAAAAAT 2231

RESULT 3
AF019048
LOCUS
DEFINITION Mus musculus receptor activator of nuclear factor kappa B ligand (RANKL) mRNA, complete cds.
ACCESSION AF019048
VERSION AF019048.1 GI:2612923
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2225)
AUTHORS Anderson,D.M., Maraskovsky,E., Billingsley,W.L., Dougall,W.C., Tomesko,M.E., Roux,E.R., Teepe,M.C., DuBoise,R.F., Cosman,D. and Galibert,L.
TITLE A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function
JOURNAL Nature 390 (6656), 175-179 (1997)
MEDLINE 98032977
REFERENCE 2 (bases 1 to 2225)
AUTHORS Anderson,D.M., Billingsley,W., Dougall,W., Maraskovsky,E., Cosman,D., DuBoise,R. and Galibert,L.
TITLE Direct Submission
JOURNAL Submitted (13-AUG-1997) Molecular Biology, Immunex Corp., 51 University St., Seattle, WA 98101, USA

FEATURES		Location/Qualifiers
source	1. .2225	/organism="Mus musculus"
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	/product="RANKL"	
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BASE COUNT	623 a 468 c 523 g 611 t	
ORIGIN		
	Query Match 97.8%; Score 2143.2; DB 12; Length 2225;	
	Best Local Similarity 99.3%; Pred. No. 0;	
	Matches 2173; Conservative 0; Mismatches 13; Indels 2; Gaps 2;	
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Db	73	TGGGTGCGCGAGGAAGGAGAACGATCGCGGAGCGGCCCGAACTCCGGCGCGCG 132
QY	121	CGCCATGCGCGGGCCAGCGAGACTACGGCAAGTACTTGGCGAGCTCGGAGGAGATGG 180
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QY	181	CAGCGCGCCGGCGTCCACACAGAGGTTCGGCTGCACCCCGCGCTTCTGCACCGGCTCC 240
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QY	241	GGCGCGCGCACCGCGCGCTCCCGCTCCATGTTCTTGGCGCTTCTGGGCTGGGACTGGG 300
Db	253	GGCGCGCGCACCGCGCGCTCCCGCTCCATGTTCTTGGCGCTTCTGGGCTGGGACTGGG 312
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QY	361	AATATCAGAAAGACAGCACTCACTGCTTTTATAGAACTCCTGAGACTCCTCAAAACGCGG 420
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Db	613	TGAGGCCCGAGCCATTTTCACACCTCACCATCAATGCTGCCAGCATCCCATCGGTTCCCA 672
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DB	673	TAAAGTCACTCTGTCTCTTTGGTACCACGATCGAGGCTGGCCCAAGATCTCTTACATGAC 732
QY	721	GTTAAGCAACGGAATACTAAGGTTAAACCAAGATGGCTTCTATTACCTGTACGCCAACAT 780
DB	733	GTTAAGCAACGGAATACTAAGGTTAAACCAAGATGGCTTCTATTACCTGTACGCCAACAT 792
QY	781	TTGCTTTCCGGCATCATGAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGT 840
DB	793	TTGCTTTCCGGCATCATGAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGT 852
QY	841	GTATGCTGTTAAACACAGCATCAAAATCCCAAGTCTCTCATAACTGATGAAGAGGGAG 900
DB	853	GTATGCTGTTAAACACAGCATCAAAATCCCAAGTCTCTCATAACTGATGAAGAGGGAG 912
QY	901	CACGAAAACTGCTCGGGCAATTCCTGAATTCCTCACTTTTATTCCTAATAATGTTGGGGATT 960
DB	913	CACGAAAACTGCTCGGGCAATTCCTGAATTCCTCACTTTTATTCCTAATAATGTTGGGGATT 972
QY	961	TTTCAAGCTCCGAGCTGGTGAAGAAATAGCATTCAGGTTCCTCAACCTTCCCTGCTGGA 1020
DB	973	TTTCAAGCTCCGAGCTGGTGAAGAAATAGCATTCAGGTTCCTCAACCTTCCCTGCTGGA 1032
QY	1021	TCGGGATCAAGATCGCACGTACTTTGGGGCTTTCAAAAGTTTCAGGACATAGACTGAGACTC 1080
DB	1033	TCGGGATCAAGATCGCACGTACTTTGGGGCTTTCAAAAGTTTCAGGACATAGACTGAGACTC 1092
QY	1081	ATTTCGTGGAACATTAAGCATGGATGCTTAGATGTTTGGAACTTCTTAAAAAATGGATG 1140
DB	1093	ATTTCGTGGAACATTAAGCATGGATGCTTAGATGTTTGGAACTTCTTAAAAAATGGATG 1152
QY	1141	ATGTCTATACATGTGTAAAGTACTTAAGACATGGCCCGCTGTATGAACCTCACAGC 1200
DB	1153	ATGTCTATACATGTGTAAAGTACTTAAGACATGGCCCGCTGTATGAACCTCACAGC 1212
QY	1201	CCTCTCTTTGAGCCTGTACAGGTGCTGATATGTTAAAGTCCATAGGTGATGTTAGATTC 1260
DB	1213	CCTCTCTTTGAGCCTGTACAGGTGCTGATATGTTAAAGTCCATAGGTGATGTTAGATTC 1272
QY	1261	ATGCTGATTACACACGGTTTACAAATTTGTAATGATTTCTTAAAGAAATGAACCAAT 1320
DB	1273	ATGCTGATTACACACGGTTTACAAATTTGTAATGATTTCTTAAAGAAATGAACCAAT 1331
QY	1321	GGGAGAGGTATTCCGATGCTTATGAAAACTTACAGCTGAGCTATGGAAGGGGTACAG 1380
DB	1332	GGGAGAGGTATTCCGATGCTTATGAAAACTTACAGCTGAGCTATGGAAGGGGTACAG 1391
QY	1381	TCTCTGGGTCTAACCCCTGGACATGCGCACTGAGAACCTTGAAATTAAGAGATGCCAT 1440
DB	1392	TCTCTGGGTCTAACCCCTGGACATGCGCACTGAGAACCTTGAAATTAAGAGATGCCAT 1451
QY	1441	GTCATTGCAAGAAATGATGCTGAAGGTTAAGTCTTCTTGAATGTTACATTGGCT 1500
DB	1452	GTCATTGCAAGAAATGATGCTGAAGGTTAAGTCTTCTTGAATGTTACATTGGCT 1511
QY	1501	GGGACTGCAAAATAGTCTTTTTTCTAATGAGGAGAGAAAAATATATGTTATTTATA 1560
DB	1512	GGGACTGCAAAATAGTCTTTTTTCTAATGAGGAGAGAAAAATATATGTTATTTATA 1571
QY	1561	TAATGCTAAAGTTATATTTCAGGTGTAATGTTTCTGTGCAAGTTTCTGTAATATAT 1620
DB	1572	TAATGCTAAAGTTATATTTCAGGTGTAATGTTTCTGTGCAAGTTTCTGTAATATAT 1631
QY	1621	TTTGTCTATAGTATTTCGATTCAAAATATTAAAAATGCTCTCAGCTGTTGACATATTAAATG 1680
DB	1632	TTTGTCTATAGTATTTCGATTCAAAATATTAAAAATGCTCTCAGCTGTTGACATATTAAATG 1691
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DB	1692	TTTTAAATCTACAGATGATTTAACTGGTGCACCTTTGTAATTCCTGGAAGGTACTCGTA 1751
QY	1741	GCTAAGGGGCGAGATACCTGTTTCTGCTGACCATGATGTTTATTTCTTTATCTTTT 1800

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QY	721	GTTAAGCAACGAAACCTAAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCAAGAT	780
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QY	781	TTCGCTTCGGGATCATGAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGT	840
Db	798	TTCGCTTCGGGATCATGAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGT	857
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QY	1201	CCTCTCTCTTGAG-CCTGTACAGGTTGTATATGTAAGTCCATAGGTGATGTTAGATT	1259
Db	1218	CCTCTCTCTTGAGCCCTGTACAGGTTGTATATGTAAGTCCATAGGTGATGTTAGATT	1277
QY	1260	CATCGTGATTACACACGGTTTACAAATTTTGAATGATTTTCCCTAAGAAATGAACACAT	1319
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QY	1320	TGGGAGAGGTATTCGGATGCTTATGAAAACTTACACGTGAGCTATGGAAGGGGTGACA	1379
Db	1337	TGGGAGAGGTATTCGGATGCTTATGAAAACTTACACGTGAGCTATGGAAGGGGTGACA	1396
QY	1380	GTCTCTGGGCTAACCCCTGGACATGTCGCCACTGAGAACCTTGAATTAAGAAGATGCCA	1439
Db	1397	GTCTCT-GGTCTAACCCCTGGACATGTCGCCACTGAGAACCTTGAATTAAGAGGATGCCA	1455
QY	1440	TGTCATTGCAAGAAATGATAGTGAAGGGTTAAGTTCCTTTGAAATTTGATATTTTAT	1499
Db	1456	TGTCATTGCAATAGAAATGATAGTGAAGGGTTAAGTTCCTTTGAAATTTGATATTTTAT	1515
QY	1500	TGGGACCTGCAATAAGTCTTTTTTCTAATGAGGAGAGAAAAATATATGATTTTAT	1559
Db	1516	TGGGACCTGCAATAAGTCTTTTTTCTAATGAG--GAGAAAAATATGATTTTAT	1573
QY	1560	ATAATGTCTAAAGTTATATTTTCAGGTGTAATGTTTTCGTGCAAGTTTCTGTAATATATA	1619
Db	1574	ATAATGTCTAAAGTTATATTTTCAGGTGTAATGTTTTCGTGCAAGTTTCTGTAATATATA	1633
QY	1620	TTTCTGCTATAGTATTTGATTCAAATATTTTAAAAATGCTCACTGTTTCACATATTTAAT	1679
Db	1634	TTTCTGCTATAGTATTTGATTCAAATATTTTAAAAATGCTCACTGTTTCACATATTTAAT	1693
QY	1680	GTTTTAAATGTACAGATGATTTTAACTGGTGCATTTTGTATATTCCTTGAAGGACTCGT	1739
Db	1694	GTTTTAAATGTACAGATGATTTTAACTGGTGCATTTTGTATATTCCTTGAAGGACTCGT	1753

QY	1740	AGCTAAGGGGCGAGAATACTGTTTCTGGTGACCACATCTAGTTTATTTCTTTATCTTTT	1799
Db	1754	AGCTAAGGGGCGAGAATACTGTTTCTGGTGACCACATCTAGTTTATTTCTTTATCTTTT	1813
QY	1800	TAACTTAATAGAGCTTTCAGACTTGTCAAAACTATGCAAGCAAAATAAATAAATAAAT	1859
Db	1814	TAACTTAATAGAGCTTTCAGACTTGTCAAAACTATGCAAGCAAAATAAATAAATAAAT	1873
QY	1860	AAATGAATATCTTGAATATAAGTAGGATGTTGGTCACCAGGTGCCTTTCAAAATTTAGA	1919
Db	1874	AAATGAATATCTTGAATATAAGTAGGATGTTGGTCACCAGGTGCCTTTCAAAATTTAGA	1933
QY	1920	AGCTAATTCACATTTAGGAGCTGACATAGCCAAAGAGATACATAATAGGCTACTGAAAAT	1979
Db	1934	AGCTAATTCACATTTAGGAGCTGACATAGCCAAAGAG-ACATAATAGGCTACTG-AAAT	1991
QY	1980	CTGTCAAGGAGTATTTATGCAATTAATTGAACAGGTGCTCTTTTACAGAGCTACAAAT	2039
Db	1992	CTGTCAAGGAGTATTTATGCAATTAATTGAACAGGTGCTCTTTTACAGAGCTACAAAT	2051
QY	2040	GTAATTTT-GTTCCTTTTTTTTCCCATAGAAATGTACTATAGTTTATCAGCCAAAAA	2098
Db	2052	GTAATTTTGGTTCCTTTTTTTTCCCATAGAAATGTACTATAGTTTATCAGCCAAAAA	2111
QY	2099	CAATCCACATTTTAAATTTAGTGAAGTTATTTATTAATGCTACATAAAGCATTTGTT	2158
Db	2112	CAATCCACATTTTAAATTTAGTGAAGTTATTTATTAATGCTACATAAAGCATTTGTT	2171
QY	2159	TCTGAATGCAATTTTGTGTTACTTAAAAAT 2188	
Db	2172	TCGAAATGTTAATTTTGTGTACAAAAAT 2201	
RESULT	5		
AB022036S4			
LOCUS	AB022036S4	2029 bp	DNA
DEFINITION	Mus musculus DNA for osteoclast differentiation factor, exon 5, complete cds.		
ACCESSION	AB022039.1	GI:4127268	
VERSION	AB022039.1	GI:4127268	
KEYWORDS	osteoclast differentiation factor.		
SEGMENT	4 of 4		
SOURCE	Mus musculus (strain:129) embryonic stem cell DNA.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Kodaira,K., Kodaira,K., Mizuno,A., Yasuda,H., Shima,N., Murakami,A., Ueda,M. and Higashio,K.		
TITLE	Cloning and characterization of the gene encoding mouse osteoclast differentiation factor		
JOURNAL	Gene 230 (1), 121-127 (1999)		
MEDLINE	99214075		
REFERENCE	2 (bases 1 to 2029)		
AUTHORS	Kodaira,K.		
TITLE	Direct Submission		
JOURNAL	Submitted (05-JAN-1999) to the DDBJ/EMBL/GenBank databases		
	Kunihiko Kodaira, YS New Technology Institute Inc., Molecular Biology, Shimoishibashi 519, Ishibashi-machi, Tohigi 329-0512, Japan (E-mail:Y.SN@et-cnet.or.jp, Tel:81-285-52-2821, Fax:81-285-52-2824)		
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	/db_xref="GI:4127270"		

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159.1043
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BASE COUNT 620 a 334 c 412 if 663 t
ORIGIN

Query Match		66.7%;	Score: 1460.8;	DB 12;	Length 2029;
Best Local Similarity		98.6%;	Pred. No. 4.5e-261;		
Matches 1515;		Conservative 0;	Mismatches 17;	Indels 4;	Gaps 4;
QY	653	GGTTCCCATAAAGTCACCTGCTCTCTT;GTACACACATCGAGGCTGGGCCAAGATCTCT	712		
Db	158	GGTTCCCATAAAGTCACCTGCTCTCTT;GTACACACATCGAGGCTGGGCCAAGATCTCT	217		
QY	713	AACATGACGTTAAAGCAACGAAACTAA;IGTTAAACCAAGATGGCTTCTATTACCTGTAC	772		
Db	218	AACATGACGTTAAAGCAACGAAACTAA;IGTTAAACCAAGATGGCTTCTATTACCTGTAC	277		
QY	773	GCCAAATTTGCTTTCGGCATCATGAAA;ATCGGGAAGCGTACCTACAGACTATCTTCAG;832			
Db	278	GCCAAATTTGCTTTCGGCATCATGAAA;ATCGGGAAGCGTACCTACAGACTATCTTCAG	337		
QY	833	CTGATGGTGTATGCTTTAAACCCAGCA;TCAAAATCCCAAGTCTCATACCTGATGAAA	892		
Db	338	CTGATGGTGTATGCTTTAAACCCAGCA;TCAAAATCCCAAGTCTCATACCTGATGAAA	397		
QY	893	GGAGGGAGCAGCAAAACTGCTCGGGCAATTCTCAATTCACACTTTTATTCATATAAATGTT	952		
Db	398	GGAGGGAGCAGCAAAACTGCTCGGGCAATTCTCAATTCACACTTTTATTCATATAAATGTT	457		
QY	953	GGGGGATTTTCAAGCTCCGAGCTGGTGAAGAAATTAGCATTTAGGTTGTCACACCCCTCC	1012		
Db	458	GGGGGATTTTCAAGCTCCGAGCTGGTGAAGAAATTAGCATTTAGGTTGTCACACCCCTCC	517		
QY	1013	CTGCTGGATCCGATCAAGATGGAGTACTTTGGGGCTTTCAAGTTCAGGACATAGAC	1072		
Db	518	CTGCTGGATCCGATCAAGATGGAGTACTTTGGGGCTTTCAAGTTCAGGACATAGAC	577		
QY	1073	TGAGACTCATTTCTGCGAACATTAGCA;GGATCTCTAGATGTTTGAACACTTCTTAAA	1132		
Db	578	TGAGACTCATTTCTGCGAACATTAGCA;GGATCTCTAGATGTTTGAACACTTCTTAAA	637		
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QY	1253	TTAGATTTCATGGTATACACACGGTTTACAAATTTTGTAAATGATTTCTTAAGAAATGA	1312		
Db	758	TTAGATTTCATGGTATACACACGGTTTACAAATTTTGTAAATGATTTCTTAAATGA	816		
QY	1313	ACCAGATTGGGAGAGTATTTCCCATGCTATGAAAACCTTACACGTCAGCTATGGAAGG	1372		
Db	817	ACCAGATTGGGAGAGTATTTCCCATGCTATGAAAACCTTACACGTCAGCTATGGAAGG	876		
QY	1373	GGTCACAGTCTCTGGGTCTAACCCCTG;ACATGTGCCACTGAGAACCTTCAAAATTAAGAA	1432		
Db	877	GGTCACAGTCTCTGGGTCTAACCCCTG;ACATGTGCCACTGAGAACCTTCAAAATTAAGAA	936		
QY	1433	GATGCCATGTCATTGCAAGAAATGAT;GTGTGAAGGGTTAAGTCTCTTTTGAATTTGATAC	1492		
Db	937	GATGCCATGTCATTGCAAGAAATGAT;GTGTGAAGGGTTAAGTCTCTTTTGAATTTGATAC	996		

QY	1493	ATTGGCGTGGACCTGCAAAATAAGTTCTTTTTTCTTAATGAGAGAGAGAAAAATATATGTA	1552		
Db	997	ATTGGCGTGGACCTGCAAAATAAGTTCTTTTTTCTTAATGAGAGAGAGAAAAATATATGTA	1056		
QY	1553	TTTTTATATAATGCTCTAAAGTTATATTTTCAGGCTGAATGTTTCTCTGCAAAAGTTTGTGA	1612		
Db	1057	TTTTTATATAATGCTCTAAAGTTATATTTTCAGGCTGAATGTTTCTCTGCAAAAGTTTGTGA	1116		
QY	1613	AATTATATTTTGTGCTATAGTATTTGATTCAAAATATTTTAAAAATGCTCAGCTGTTGCACAT	1672		
Db	1117	AATTATATTTTGTGCTATAGTATTTGATTCAAAATATTTTAAAAATGCTCAGCTGTTGCACAT	1176		
QY	1673	ATTTAATGTTTTAAATGTCAGATGATTTTAACTGGTGACACTTTGTAAATTCCTCCGGAAGG	1732		
Db	1177	ATTTAATGTTTTAAATGTCAGATGATTTTAACTGGTGACACTTTGTAAATTCCTCCGGAAGG	1235		
QY	1733	TACTGCTAGCTTAAGGGGCGAGAATACTGTTCTGTTGTCAGGACCATGATAGTTTATTTCTTTA	1792		
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QY	1793	TTCTTTTAACTTAATAGAGTCTTCAGACTTGTCAAAAATGTCAGGACCAAAATAATAAA	1852		
Db	1296	TTCTTTTAACTTAATAGAGTCTTCAGACTTGTCAAAAATGTCAGGACCAAAATAATAAA	1355		
QY	1853	TAAAAATAAAATGAATATCTTGAATAATAAGTAGGATGTTGGTCACCGAGTGCCTTTTCAA	1912		
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QY	1973	TGAAAACTGTCAGAGTATTTATGCAATTTATGAACAGGTGCTCTTTTTTACAGAGCT	2032		
Db	1476	TGAAAACTGTCAGAGTATTTATGCAATTTATGAACAGGTGCTCTTTTTTACAGAGCT	1534		
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Db	1535	ACAAATTTGTAATTTTCTTTTCCCATAGAAAAATGTTACTATAGTTTATTCAGC	1594		
QY	2092	CAAAAAACAATCCACTTTTTTAAATTTAGTGAAGTTATTTTATTTATACATAAATAAG	2151		
Db	1595	CAAAAAACAATCCACTTTTTTAAATTTAGTGAAGTTATTTTATTTATACATAAATAAG	1654		
QY	2152	CATTGTTTCTCAATGGCATTTTTTGGTACTTAAAAA	2187		
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RESULT 6

AF053712	2271 bp	mRNA	PRI	09-MAY-1998
LOCUS				
DEFINITION Homo sapiens osteoprotegerin ligand mRNA, complete cds.				
ACCESSION AF053712				
VERSION AF053712.1 GI:3057145				
KEYWORDS				
SOURCE human.				
ORGANISM				
Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE				
AUTHORS				
1 (bases 1 to 2271)				
Lacey,D.L., Timms,E., Tan,H.-L., Kelley,M.J., Dunstan,C.R.,				
Burgess,T., Elliott,R., Colombero,A., Elliott,G., Scully,S.,				
Hsu,H., Sullivan,J., Hawkins,N., Davy,E., Capparelli,C., Eli,A.,				
Qian,Y.-X., Kaufman,S., Sarosi,I., Shalhoub,V., Senaldi,G., Guo,J.,				
Delaney,J., and Boyle,W.J.				
TITLE				
Osteoprotegerin ligand is a cytokine that regulates osteoclast				
differentiation and activation				
JOURNAL				
MEDLINE				
Cell 93 (2), 165-176 (1998)				
REFERENCE				
2 (bases 1 to 2271)				
Boyle,W.J.				
TITLE				
Direct Submission				

JOURNAL	Submitted (16-WAR-1998)	Department of Cell Biology, Amgen, Inc., One Amgen Center Drive, Thousand Oaks, California 91320, USA
FEATURES	Location/Qualifiers 1..2271	
source	/organism="Homo sapiens" /db_xref="taxon:9606"	
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Qy	96 CAGGCGCCCCGAACCTCCGGCGCC--CGCCATCGCGCGCGGCACGCGAGACTACGGCAA 153	
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Db	811	TCAGGATGSCCTTTATTACCTGTATGCCAACATTTGCTTTTCGACATCATGNAACTTCAGG	870
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Db	871	AGACCTAGCTACAGAGTATCTTCCAGCTAATGGTGTAGCTCACTAAAAACGACATCAAAAT	930
Qy	868	CCCAAGTTCTCATAACTGATGAAGAGGAGGACACGAAAAAAGCTGTCGGCAATTCCTGA	927
Db	931	CCCAAGTTCTCATACCCTGATGAAGAGGAGGAGCAACCAAGTATTTGGTCAGGGAATTCCTGA	990
Qy	928	ATTCCACTTTTATTCCTAAATGTTGGGGGATTTTTCAAGCTCCCGAGCTGGTGAAGAAAT	987
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Qy	988	TAGCATTTAGGTGTCCAACCCCTTCCCTGCHGGATTCGGGATCAAGATCGGAGGTACTTTGG	1047
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Qy	1048	GGCTTTCRAAGTTCAGGACATAGACTCAGACTCATTTCTGTTGGAACATTAGCATGGATGC	1107
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Db 2083 -TTTTTTTTTTCAAAATAGAAAGTTAT/AGTGGTTTATCAGCAAAAAGTCCAAATTT 2141
QY 2113 ATTAGTGAAGTTATTTTATATACTG/ACATAAAAGCATTTGTTTCTGAATGGCATTT 2172
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QY 2173 TTTGGTACTTAAAA 2186
Db 2199 TTTTGGTACAAAAA 2212

RESULT 7
AF019047 2201 bp mRNA PRI 22-NOV-1997
LOCUS Homo sapiens receptor activator of nuclear factor kappa B ligand
DEFINITION (RANKL) mRNA, complete cds.
ACCESSION AF019047
VERSION AF019047.1 GI:2612921
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2201)
AUTHORS Anderson,D.M., Maraskovsky,E., Billingsley,W.L., Dougall,W.C.,
Tometsko,M.E., Roux,E.R., Teepe,M.C., DuBose,R.F., Cosman,D. and
Galibert,L.
TITLE A homologue of the TNF receptor and its ligand enhance T-cell
growth and dendritic-cell function
JOURNAL Nature 390 (6556), 175-179 (1997)
MEDLINE 98032977
AUTHORS Anderson,D.M., Billingsley,W., Dougall,W., Maraskovsky,E.,
Cosman,D., DuBose,R. and Galibert,L.
TITLE Direct Submission
JOURNAL Submitted (13-AUG-1997) Molecular Biology, Immunex Corp., 51
University St., Seattle, WA, 98101, USA
FEATURES
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QY 748 CCAAGATGGCTTCTATTACCTGTACGCCCAACATTTGCTTTGGGCATCATGAACATCGGG 807
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QY 868 CCCAAGTCTCATAACTGATGAAGGAGGAGGAGCAGCAAAACACTGTCGGGCAATCTGCA 927
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RESULT 8
AF013171 1823 bp mRNA PRI 19-SEP-1997
LOCUS AF013171 Homo sapiens TNF-related ligand TRANCE mRNA, partial cds.
DEFINITION AF013171
ACCESSION AF013171
VERSION AF013171.1 GI:2411499
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1823)
AUTHORS Wong,B.R., Rho,J., Arron,J., Robinson,E., Orlicki,J., Chao,M.,
Kalachikov,S., Cayani,E., Bartlett,F.S. III, Frankel,W.N., Lee,S.Y.
and Choi,Y.
TITLE TRANCE is a novel ligand of the tumor necrosis factor receptor
family that activates c-Jun N-terminal kinase in T cells
J. Biol. Chem. 272 (40), 25190-25194 (1997)
MEDLINE 97460112
REFERENCE 2 (bases 1 to 1823)
AUTHORS Wong,B.R., Rho,J., Arron,J., Lee,S.Y., Robinson,E. and Choi,Y.
Direct Submission
TITLE Submitted (09-JUL-1997) Howard Hughes Medical Institute, The
Rockefeller University, 1230 York Ave., New York, NY 10021, USA
FEATURES
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AUTHORS	Yasuda,H., Shima,N., Nakagawa,N., Yamaguchi,K., Kinoshita,M., Morizuki,S., Tomoyasu,A., Yano,K., Goto,M., Murakami,A., Tsuda,E., Morinaga,T., Higashi,K., Udagawa,N., Takahashi,N. and Suda,T.
TITLE	Osteoclast differentiation factor is a ligand for osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical to TRANCE/RANKL
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3597-3602 (1998)
MEDLINE	98188248
FEATURES	Location/Qualifiers 1. .951 /organism="Mus musculus" /db_xref="taxon:10090" /cell_line="St2" /cell_type="stromal cells" /clone="pOBM291" /clone_lib="pcDL-Sra296" /tissue_type="bone marrow" 1. .951 /codon_start=1 /product="osteoclast differentiation factor (ODF)" /protein_id="BAA25425.1" /db_xref="GI:3041782" /translation="MRRASRDYGVKLYLRSEEMSGPGVPHEGPLHPAPSAPAPAPDA ASRFLALLGLGVGVCSIALFLYFRQMDPNRISDSSTHCFYILRLHENGAGLDD STLESSEDTLPDSCRMKQAFQAVQKELHIIVGPQPSGAPAMFEGSLDVAQGRKE AOPFAHLTINAASIFSGSHKVISSWYHGRWAKITSNMTLSNGKLKRVNQGYLYXAN ICFRHEHTSGSVPTDYQLQMLVYVVKTSIKIPSHNLMLKGGSTKNWGSNSEHFYYSIN GGFFKLRCAGEEISIQVSNPSSLDDPDQDQATYFGAFKVDID" 142. 213 /note="transmembrane domain" 454. 948 /note="Tumor Necrosis Factor(TNF)-like domain"
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QY	305 GTGGTCTGCAGCATCGCTCTGTTCTCTACTTTCGACCGCAGATGGATCTTAACAGAAATA 364
Db	 181 GTGGTCTGCAGCATCGCTCTGTTCTCTACTTTCGACCGCAGATGGATCTTAACAGAAATA 240
QY	365 TCAGAAGACAGCACTCACTGCTTTTATAGAAATCCTGAGACTTCCATGAAACGCAAGTTTG 424
Db	 241 TCAGAAGACAGCACTCACTGCTTTTATAGAAATCCTGAGACTTCCATGAAACGCAAGTTTG 300
QY	425 CAGGACTCGACTCGGAGAGTGAAGACACACTACCTGACTCTCTCGAGGAGGATGAAACAA 484
Db	 301 CAGGACTCGACTCGGAGAGTGAAGACACACTACCTGACTCTCTCGAGGAGGATGAAACAA 360
QY	485 GCCTTTTCAGGGGGCGGTGCAGAGGAAGACTGCAACACATTTGTGGGGCCACACGCTTCTCA 544
Db	 361 GCCTTTTCAGGGGGCGGTGCAGAGGAAGACTGCAACACATTTGTGGGGCCACACGCTTCTCA 420
QY	545 GGAGCTCCAGCTATGATGGAAGGCTCATGTTGGATGTGGCCCGCAGCGAGGCAACGCTTGA 604
Db	 421 GGAGCTCCAGCTATGATGGAAGGCTCATGTTGGATGTGGCCCGCAGCGAGGCAACGCTTGA 480
QY	605 GCCCAGCGCAATTTGCACACCTTCACCATCAATGCTGCCAGCATCCCATCGGTTCCCATAAA 664

Db	481	GCACAGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCGGGTCCCATAAA	540
Qy	665	GTCACTCTGTCTCTTGGTACACGATCGAGCTGGGCCAAGATCTCTAACATGACGTTA	724
Db	541	GTCACTCTGTCTCTTGGTACCAGATCGAGCTGGGCCAAGATCTCTAACATGACGTTA	600
Qy	725	AGCAACGGAAACAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCAACATTTGC	784
Db	601	AGCAACGGAAACAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCAACATTTGC	660
Qy	785	TTTCGGCATCATGNAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGTGTAT	844
Db	661	TTTCGGCATCATGNAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGTGTAT	720
Qy	845	GTCTGTTAAACACAGCATCAAAATCCCAAGTTCCTCATAACTGATGAAGAGGAGGACGACG	904
Db	721	GTCTGTTAAACACAGCATCAAAATCCCAAGTTCCTCATAACTGATGAAGAGGAGGACGACG	780
Qy	905	AAAACTGGTGGGCAATCTGAATCCACTTTTATTCATAAATGTTGGGGGATTTTTC	964
Db	781	AAAACTGGTGGGCAATCTGAATCCACTTTTATTCATAAATGTTGGGGGATTTTTC	840
Qy	965	AAGTCCGAGCTGTTGAAGAAATTAGCATTCAGTGTCCAAACCTTCCTGCTGGATCCG	1024
Db	841	AAGTCCGAGCTGTTGAAGAAATTAGCATTCAGTGTCCAAACCTTCCTGCTGGATCCG	900
Qy	1025	GATCAAGATCGACGTACTTTGGGGCTTTCAAACTTCAGGACATAGACTGA	1075
Db	901	GATCAAGATCGACGTACTTTGGGGCTTTCAAACTTCAGGACATAGACTGA	951
RESULT 10			
AB036798			
LOCUS	AB036798	951 bp	mRNA
DEFINITION	Mus musculus mRNA for RANKL 1, complete cds.		
ACCESSION	AB036798		
VERSION	AB036798.1		
KEYWORDS	RANKL 1.		
SOURCE	Mus musculus		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
JOURNAL	TITLE		
REFERENCE	RANKL 1		
AUTHORS	Ikeda, T.		
JOURNAL	Published Only in DataBase (2000) In press		
TITLE	2 (bases 1 to 951)		
JOURNAL	Ikeda, T.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (11-JAN-2000) to the DDBJ/EMBL/GenBank databases. Tooru		
JOURNAL	Ikeda, School of Medicine, Tokyo Medical and Dental University,		
TITLE	Department of Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku,		
JOURNAL	Tokyo 113-8519, Japan (E-mail: toru.pth2@med.tmd.ac.jp,		
REFERENCE	Tel:81-3-5803-5176, Fax:81-3-5803-0123)		
AUTHORS	Location/Qualifiers		
JOURNAL	1. 951		
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SOURCE	/db_xref="taxon:10090"		
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	AQPFAHLLTNAASIPGSHKVTLLSNWYHDKRAKISNMTLSNGKLRVNDGFYLVAN		
	ICFRHETSSVPTDYDLYLMVYVVKTSIKIPSSHNLKMGGSTKNWSGNSSEHFYSIN		
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BASE COUNT	231 a	267 c	248 g 205 t

ORIGIN

Query Match 43.4%; Score 951; DB 12; Length 951;
Best Local Similarity 100.0%; Prec. No. 1.4e-166;
Matches 951; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 125 ATGCGCGGGCCAGCGAGACTAGGCA GTACCTGCGAGCTCGGAGGAGTGGCGAGC 184
DB 1 ATGCGCGGGCCAGCGAGACTAGGCA GTACCTGCGAGCTCGGAGGAGTGGCGAGC 60

QY 185 GCGCCCGGGTCCACACAGAGGTGCGCTGCACCCGCGCTTCTGCACCGCTCCGGCG 244
DB 61 GCGCCCGGGTCCACACAGAGGTGCGCTGCACCCGCGCTTCTGCACCGCTCCGGCG 120

QY 245 CGCCACCGCGCGCTCCCGCTCCATGTT CCGGGCCCTTCCTGGGCTGGGACTGGGCCAG 304
DB 121 CGCCACCGCGCGCTCCCGCTCCATGTT CCGGGCCCTTCCTGGGCTGGGACTGGGCCAG 180

QY 305 GTGGTCTGAGCATCGCTCTGTTCCTGTACTTTCGAGCGCAGATGATCTTAACAGATA 364
DB 181 GTGGTCTGAGCATCGCTCTGTTCCTGTACTTTCGAGCGCAGATGATCTTAACAGATA 240

QY 365 TCAGAGACAGCACTCACTGCTTTTATAGAACTCTGAGACTCCATGAACACGAGTTTG 424
DB 241 TCAGAGACAGCACTCACTGCTTTTATAGAACTCTGAGACTCCATGAACACGAGTTTG 300

QY 425 CAGGACTCGACTCTGGAGAGTGAAGACAC ACTACCTGACTCTCTGCAGGAGGATGAACAA 484
DB 301 CAGGACTCGACTCTGGAGAGTGAAGACAC ACTACCTGACTCTCTGCAGGAGGATGAACAA 360

QY 485 GCCTTTCAGGGGCGGTGCAAGAGAACTGCAACACATTGTGGGGCCACACGCTTCTCA 544
DB 361 GCCTTTCAGGGGCGGTGCAAGAGAACTGCAACACATTGTGGGGCCACACGCTTCTCA 420

QY 545 GGAGCTCCAGCTATGATGAAGCTCATGTTGGATGTGCCAGCATCCATCGGGTTCCTCAAA 664
DB 421 GGAGCTCCAGCTATGATGAAGCTCATGTTGGATGTGCCAGCATCCATCGGGTTCCTCAAA 480

QY 605 GCCAGCCATTTGCACACCTCAACATCAATGTGTCGCCAGCATCCATCGGGTTCCTCAAA 664
DB 481 GCCAGCCATTTGCACACCTCAACATCAATGTGTCGCCAGCATCCATCGGGTTCCTCAAA 540

QY 665 GTCACCTCTGCTCTTGGTACACAGATCGAGGTGGGGCCAGATCTCTAACATGAGCTTA 724
DB 541 GTCACCTCTGCTCTTGGTACACAGATCGAGGTGGGGCCAGATCTCTAACATGAGCTTA 600

QY 725 AGCAACGGAATAAGGTTAACCAGATGGCTTCTATTACCTGTACGCCACATTTGC 784
DB 601 AGCAACGGAATAAGGTTAACCAGATGGCTTCTATTACCTGTACGCCACATTTGC 660

QY 785 TTTCCGSCATCATGAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGTGTAT 844
DB 661 TTTCCGSCATCATGAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGTGTAT 720

QY 845 GTCGTTAAACAGCATCAAAATCCCAAGTTCATACCTGATGAAGAGGAGGACACG 904
DB 721 GTCGTTAAACAGCATCAAAATCCCAAGTTCATACCTGATGAAGAGGAGGACACG 780

QY 905 AAAAAGTGTGCGGCAATTCGAAATCCCACTTTTATTCATTAATGTTGGGGATTTTC 964
DB 781 AAAAAGTGTGCGGCAATTCGAAATCCCACTTTTATTCATTAATGTTGGGGATTTTC 840

QY 965 AAGCTCCGAGCTGGTGAAGAAATTAAGCATTCAGGTGTCACACCTTCCTGCTGGATCCG 1024
DB 841 AAGCTCCGAGCTGGTGAAGAAATTAAGCATTCAGGTGTCACACCTTCCTGCTGGATCCG 900

QY 1025 GATCAAGATGCGACGTACTTTGGGGTTTCAAAGTTTCAGGACATAGACTGA 1075
DB 901 GATCAAGATGCGACGTACTTTGGGGTTTCAAAGTTTCAGGACATAGACTGA 951

RESULT 11

AB032771 864 bp mRNA ROD 29-JUN-2000
LOCUS Mus musculus RANKL 2 mRNA for receptor activator of NF-kB ligand 2,
DEFINITION complete cds.
ACCESSION AB032771
VERSION AB032771.1 GI:8843822
KEYWORDS receptor activator of NF-kB ligand 2.
SOURCE Mus musculus
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
Ikeda,T.
TITLE Receptor activator of NF-kB ligand 2
JOURNAL Published Only in DataBase (2000) In press
REFERENCE 2 (bases 1 to 864)
AUTHORS Ikeda,T.
TITLE Direct Submission
JOURNAL Submitted (28-SEP-1999) to the DDBJ/EMBL/GenBank databases. Tohru
Ikeda, School of Medicine, Tokyo Medical and Dental University,
Department of Pathology and Immunology, 1-5-45 Yushima, Bunkyo-ku,
Tokyo 113-8519, Japan (E-mail:toru.pth@med.tmd.ac.jp,
Tel:81-3-5803-5176; Fax:81-3-5803-0123)
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/db_xref="taxon:10090"
gene 1..864
/gene="RANKL 2"
CDS 1..864
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BASE COUNT 221 a 227 c 219 g 197 t
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Query Match 37.3%; Score 818.2; DB 12; Length 864;
Best Local Similarity 99.0%; Pred. No. 5.6e-142;
Matches 823; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 245 CGCCACCGCGCGCTCCCGCTCCATGTTCTCTGGCCCTCTCTGGGCTGGGACTGGGCCAG 304
DB 34 CTGCGCACTCCGGCGTCCGCTCCATGTTCTGCGCCCTCTCTGGGCTGGGACTGGGCCAG 93

QY 305 GTGGTCTGAGCATCGCTCTGTTCTCTACTTTTCGAGCGCAGATGGATCTTAACAGATA 364
DB 94 GTGGTCTGAGCATCGCTCTGTTCTCTACTTTTCGAGCGCAGATGGATCTTAACAGATA 153

QY 365 TCAGAGACAGCACTCACTGCTTTTATAGATCTCTGAGACTCCATGAACACGAGTTTG 424
DB 154 TCAGAGACAGCACTCACTGCTTTTATAGATCTCTGAGACTCCATGAACACGAGTTTG 213

QY 425 CAGGACTCGACTCTGGAGAGTGAAGACACACTACTCTGACTCTCTCAGAGGATGAACAA 484
DB 214 CAGGACTCGACTCTGGAGAGTGAAGACACACTACTCTGACTCTCTCAGAGGATGAACAA 273

QY 485 GCCTTTTCAGGGGCGGTGCAAGAGAACTGCAACACATTGTGGGGCCACACGCTTCTCA 544
DB 274 GCCTTTTCAGGGGCGGTGCAAGAGAACTGCAACACATTGTGGGGCCACACGCTTCTCA 333

QY 545 GGAGCTCCAGCTATGATGAAGGCTCATGTTGGATGTGGCCCGCAGCGGCAACGCTGAG 604
DB 334 GGAGCTCCAGCTATGATGAAGGCTCATGTTGGATGTGGCCCGCAGCGGCAACGCTGAG 393

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* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 19230: contig of 19230 bp in length
19231 19330: gap of 100 bp
19331 32371: contig of 13041 bp in length
32372 32471: gap of 100 bp
32472 34870: contig of 2399 bp in length
34871 34970: gap of 100 bp
34971 42014: contig of 7044 bp in length
42015 42114: gap of 100 bp
42115 50153: contig of 8039 bp in length
50154 50253: gap of 100 bp
50254 56692: contig of 6439 bp in length
56693 56792: gap of 100 bp
56793 61250: contig of 4458 bp in length
61251 61350: gap of 100 bp
61351 62561: contig of 1211 bp in length
62562 62661: gap of 100 bp
62662 75173: contig of 12512 bp in length
75174 75273: gap of 100 bp
75274 81438: contig of 6165 bp in length
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87286 87385: gap of 100 bp
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89591 89690: gap of 100 bp
89691 91525: contig of 1835 bp in length
91526 91625: gap of 100 bp
91626 106940: contig of 15315 bp in length
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* NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces

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fragment_chain:1"
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ORIGIN
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Best local Similarity 76.3%; Pred. No. 2.2e-133;
Matches 1190; Conservative 0; Mismatches 302; Indels 67; Gaps 17;

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Db 135083 CTTCTCCACAGGTTCCCAATAAGTCACTCTGTCTCTCTTTGGTACCACGATCGAGGTGGGC 135142

Qy 703 CAAGATCTCTAACATGAGCTTAAGCAACGGAACCTAAGGGTTTAACCAAGATGGGTCTCTA 762
Db 135143 CAAGATCTCCACATGACTTTTAGCAATGGAAACTATATAGTAAATCAGGATGGCTTTTA 135202

Qy 763 TTACCTGTAGCCCAACATTTCTTTCGCATCATGAAACATCGGGAAGCGTACCTACAGAGA 822
Db 135203 TTACCTGTATGCCAACATTTCTTTCGCATCATGAAACCTTCAGGAGACCTAGCTACAGA 135262

Qy 823 CTATCTTCAGCTGATGGTGTATGTCGTTTAAACACAGCATCAAAATCCCAAGTCTCTCATAA 882
Db 135263 GTATCTTCACTAATGTTGTACGTCACTTAAACACAGCATCAAAATCCCAAGTCTCTCATAA 135322

Qy 883 CCTGATGAAAGGAGGACGACGCAAAACTGGTCGGGCAATCTGAATTCCTACTTTTATTC 942
Db 135323 CCTGATGAAAGGAGGAGGACGACCAAGTATTGGTCAGGGAATTTCTGAATTTCCATTTTATTC 135382

Qy 943 CATAAATGTTGGGGATTTTTTCAAGCTCCGAGCTGGTGAAGAAATTAGCATTTACAGTGTCTC 1002
Db 135383 CATAAAGCTTGGTGGATTTTTTAAAGTTACGCTCTGGAGAGGAAATCAGCATCGAGGTCTC 135442

Qy 1003 CAACCCCTTCCCTGCTGGATCCGGATCAAGATGCGACGACTTTTGGGGCTTTCAAAAGTTCA 1062
Db 135443 CAACCCCTCTTACTGGATCCGGATCAGGATGCAACATACTTTGGGGCTTTTAAAGTTCCG 135502

Qy 1063 GGACATAGACTGACACTCATTTTCGTGGACATTAGCATGGATGTCCTAGATGTTTGGAAA 1122
Db 135503 AGATATAGATTGAGCCCCAGTTTTTGGAGTGT---ATGTATTCTCGTGGATGTTTGGAAA 135559

Qy 1123 CTTCTTAAAAA-----ATGGATGATGCTCATACATCTGTAAGACTACTAAGACACATG 1175
Db 135560 CATTTTTTAAACAAGCCCAAGAAAGATGATATAGGCTGTGAGACTACTAAGAGCGCATG 135619

Qy 1176 GCCACCGGTGATGAAACTCACAGCCCTCTCTCTTGAGCCCTGTACAGGTGTGTATATGT 1235
Db 135620 GCCCAACCGGTACACGACTCAGTATCCATGCTCTTGACCTGTAGAGAACACGCGTATTT 135679

Qy 1236 AAGTCCATAGCTGATGTTAGATTCATGGTG-ATTACACACGGTTTACAAATTTTGTAA 1294
Db 135680 ACAGCCAGTGGGAGATGTTAGACTCATGGTGTGTACACAATGGTTTTTAAATTTTGTAA 135739

Qy 1295 TGATTTCTTAAGAAATGAAACAGATTGGGAGAGGTATTTCGATGCTTATGAAAACCTAC 1354
Db 135740 TGAATTCCT-AGAATTAACCCAGATTGGAGCAATTCGCGGTGACCTTATGAGAACTGC 135798

Qy 1355 ACGTGAGCTATGGAAGGGGTGCACAGTCTCTGGGTCTTAACCCCTCGACATGTGCCACTGA 1414
Db 135799 ATGTGGGCTATGGGAGGG-----TTGGTCCCTGGTGTGTCGCCCTTC 135842

Qy 1415 GAACCTTGAAATTAAGAAGATGCCATGTCATTGCAAAAGAAATGATGATGTTGAAGGTTAA 1474
Db 135843 GCAGC-TGAAGTGGAGAGGGGTGCATCT-AGCGCAATTTGAAGGATCATCTGAAGGGGCAA 135900

Qy 1475 GTTCTTTTGAATTTGATGTCGCTGGAGCTGCAATAAGTCTTTTTTCTTAATGAG 1534
Db 135901 ATTCTTTTGAATTTGATGTCGCTGGAGCTGCAATAAGTCTTTTTTCTTAATGAG 135957

Qy 1535 GAGAGAAAATATATGATTTTTTATATATGCTTAAAGCTTATATTTACAGGTGTAATGTTT 1594
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Db 136137 TTGTAATTCCTCCCTGGGGAACACTTGCAGCTAAGCAGGGGAATAATCTTCTTCCCTAAT 136196
QY 1770 ACCACATGTAAGTTAATTCCTTATCTTTTAACTTAATAGA-GTCTTCAGACTTGTCAA 1828
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Db 136197 ATCAATGTCAGTATATTTCTTCTGTTCTTTTAACTTAATAGATTTTTCAGACTTGTCAA 136256
QY 1829 AACTATCCAAGCAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1888
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Db 136257 GCCTGTGC-----AAAAAATTAATAATGATGCTTGAATAATAAGCAGGA 136302
QY 1889 TGTGGTCCACGAGTGCTTCAATTTAGAACTAATTTGACTTTAG-GAGCTGACATAG 1947
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QY 1948 CCAAAAAGGATACATAATAGGCTACTGAAAATCTGTGAGGAGATTTATGCAATTTATTTGA 2007
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RESULT 13
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LOCUS AB032772 754 bp mRNA ROD 29-JUN-2000
DEFINITION Mus musculus RANKL 3 mRNA for receptor activator of NF-kB ligand 3, complete cds.
ACCESSION AB032772
VERSION AB032772.1 GI:8843824
KEYWORDS receptor activator of NF-kB ligand 3.
SOURCE Mus musculus cDNA to mRNA.
ORGANISM Mus musculus
REFERENCE 1 (sites)
AUTHORS Ikeda,T., Takahashi,H. and Hirokawa,K.
TITLE Somatostatin, a new marker of osteoblast, regulates the expression of RANKL isoforms
JOURNAL Unpublished (1999)
REFERENCE 2 (bases 1 to 754)
AUTHORS Ikeda,T.
TITLE Direct Submission
JOURNAL Submitted (28-SEP-1999) to the DDBJ/EMBL/Genbank databases. Tohru Ikeda, School of Medicine, Tokyo Medical and Dental University, Department of Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8519, Japan (E-mail:toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)
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BASE COUNT 209 a 190 c 185 g 170 t
ORIGIN
Query Match 33.1%; Score 726; DB 12; Length 754;
Best Local Similarity 100.0%; Pred. No. 6.8e-125;
Matches 726; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 350 GATCTCAACAGAAATATCAGAAGACACACTCACTGCTTTTATAGAAATCTCTGAGACTCCAT 409
Db 29 GATCTCAACAGAAATATCAGAAGACACACTCACTGCTTTTATAGAAATCTCTGAGACTCCAT 88
QY 410 GAAAACGCGAGGTTTCAGGACTCGACTCTGGAGAGTGAAGACACACTTACCTGACTCCTGTC 469
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QY 470 AGGAGGATGAAACAAGCCCTTTTCAGGGGGCGCTGCAGAAAGGAAGTGCACAACACATTTGTGGG 529
Db 149 AGGAGGATGAAACAAGCCCTTTTCAGGGGGCGCTGCAGAAAGGAAGTGCACAACACATTTGTGGG 208
QY 530 CCACAGCGCTTCTCAGGAGCTCCAGCTATGATGGAAGGCTCATGCTGGTGGATGTGGCCAG 589
Db 209 CCACAGCGCTTCTCAGGAGCTCCAGCTATGATGGAAGGCTCATGCTGGTGGATGTGGCCAG 268
QY 590 CGAGCAAGCCCTGAGGCCCGAGCCATTTGCACACCTCACCACATCAATGCTGCCAGCATCCCA 649
Db 269 CGAGCAAGCCCTGAGGCCCGAGCCATTTGCACACCTCACCACATCAATGCTGCCAGCATCCCA 328
QY 650 TCGGGTTCCCAATAAGTCACTCTGCTCTCTTGGTACCACGATCGAGGCTGGGCCAAGATC 709
Db 329 TCGGGTTCCCAATAAGTCACTCTGCTCTCTTGGTACCACGATCGAGGCTGGGCCAAGATC 388
QY 710 TCTAATCATGACGTTTAAGCAACGGAAAACTAAGGGTTTAAACCAAGATGGCTTCTATTACCTG 769
Db 389 TCTAATCATGACGTTTAAGCAACGGAAAACTAAGGGTTTAAACCAAGATGGCTTCTATTACCTG 448
QY 770 TACGCCAACATTTGCTTTCGGCATCATGAACAATCGGGAAGCGTACCTACAGACTATCTT 829
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RESULT 14
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LOCUS AC023297 113451 bp DNA HTG 03-MAR-2000
DEFINITION Homo sapiens clone RP11-21H9, WORKING DRAFT SEQUENCE, 13 unordered pieces.
ACCESSION AC023297
VERSION AC023297.3 GI:7144965

HTG: HTGS_PHASE1; HTGS_DRAFT.
human.
Source
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

Anderson, S., Baldwin, J., Berna, N., Beda, F., Boguslavsky, L., Boukhgatter, B., Brown, A., Eukett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Cdge, S., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Hearford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Laricque, K., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrum, J., Meneus, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., C'Donnell, P., O'Neil, D., Olivari, T.M., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

TITLE
JOURNAL
COMMENT

Direct Submission
Submitted (11-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 3, 2000 this sequence version replaced gi:7139552.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4020
Center clone name: 21-H-9
----- Summary Statistics
Sequencing vector: M13; W7815; 100% of reads
Chemistry: dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 106493 bases at least Q40
Consensus quality: 109791 bases at least Q30
Consensus quality: 111178 bases at least Q20
Insert size: 138000; agarose-fp
Insert quality: 112251; sun-of-contrigs
Quality coverage: 3.5 in Q20 bases; agarose-fp
Quality coverage: 4.3 in Q20 bases; sum-of-contrigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 2264: contig of 2264 bp in length
* 2265 2364: gap of 100 bp
* 2365 6779: contig of 4415 bp in length
* 6780 6879: gap of 100 bp
* 6880 11332: contig of 4453 bp in length
* 11333 11432: gap of 100 bp
* 11433 17335: contig of 5903 bp in length

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 28, 2000, 17:45:45 ; Search time 109.14 Seconds
(without alignments)
7541.478 Million cell updates/sec

Title: US-08-989-362-1
Perfect score: 2191
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2191	100.0	2191	V41489	Nucleotide sequenc
2	2144.8	97.9	2295	19 V70284	Human osteoprotege
3	2144.8	97.9	2299	21 299966	DNA encoding a mur
4	2049.2	93.5	2237	20 X80224	Murine TRANCE enco
5	1615.8	73.7	1630	19 V41377	NF-kB receptor act
6	1615.8	73.7	1630	19 V41371	NF-kB receptor act
7	1525.4	69.6	1538	19 V69886	Nucleic acid encod
8	1118.8	51.1	2271	21 299964	DNA encoding a hum
9	1118.8	51.1	2274	19 V70285	Human osteoprotege
10	957.2	43.7	1823	20 X80223	Human TRANCE encod
11	951	43.4	951	19 V69900	Nucleotide sequenc
12	951	43.4	951	21 299965	DNA encoding a mur

13	951	43.4	951	21	249024	Osteoclast formati
14	735	33.5	735	19	V69898	Nucleic acid encod
15	666.2	30.4	954	19	V41378	NF-kB receptor act
16	666.2	30.4	954	19	V41372	NF-kB receptor act
17	663	30.3	954	19	V69887	Nucleic acid encod
18	519	23.7	741	19	V69899	Nucleic acid encod
19	313.2	14.3	564	21	299967	DNA encoding a syn
20	312.2	14.2	519	21	299968	DNA encoding a syn
21	312.2	14.2	519	21	299969	DNA encoding a mur
22	278.6	12.7	519	21	299972	DNA encoding osteo
23	262.4	12.0	546	21	299971	DNA encoding osteo
24	259.4	11.8	519	21	299973	DNA encoding osteo
25	247.6	11.3	564	21	299970	DNA encoding osteo
26	120.6	5.5	254	20	X56001	Human tumour necro
27	58.4	2.7	846	19	V42205	TNF-related apopto
28	58.4	2.7	1042	18	T72796	Novel cytokine Apo
29	58.4	2.7	1042	20	X86987	Human Apo-2 ligand
30	58.4	2.7	1042	21	A07425	Human Apo-2 ligand
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32	58.4	2.7	1521	18	T72851	Truncated apoptosi
33	58.4	2.7	1521	19	V29519	Human TRAIL deleti
34	58.4	2.7	1643	18	T85210	cDNA encoding huma
35	58.4	2.7	1751	18	T72847	Human apoptosis in
36	58.4	2.7	1751	19	V29518	Human TRAIL polype
37	58.4	2.7	1769	19	V63096	Human TL2 cDNA. H
38	54.8	2.5	774	21	299985	Primer used to amp
39	54	2.5	1366	18	T72848	Mouse apoptosis in
40	54	2.5	1366	19	V29520	Murine TRAIL polyp
41	54	2.5	3048	19	V15294	Murine AGP-1 encod
42	52.8	2.4	876	19	V42206	TNF-related apopto
43	51.4	2.3	8220	16	O83529	P. falciparum Proj
44	51.4	2.3	8220	18	T72897	Plasmodium Proj3 g
45	51.4	2.3	8220	21	298286	P. falciparum Proj

ALIGNMENTS

RESULT 1
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ID V41489 standard; cDNA; 2191 BP.
XX V41489;
AC V41489;
DT 24-SEP-1998 (first entry)
XX Nucleotide sequence of mouse 499E9 gene.

XX Mouse 499E9 protein; polarised Th1 T cell; immune cell; apoptosis;
antagonist; autoimmune disorder; rheumatoid arthritis;
KW systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis;
KW acute inflammatory response; antibody; antigen; cancer; ss.
XX Mus sp.

XX Key Location/Qualifiers
FH 125..1072
FT CDS /*tag= a
FT /*product= "mouse 499E9 protein"

XX WO9825958-A2.

XX 18-JUN-1998.

XX 12-DEC-1997; 97WO-US22766.

XX 13-DEC-1996; 96US-0032846.

XX (SCHE) SCHERING CORP.

XX Gorman DM, Mattson JD;

XX WPI; 1998-348452/30.

DR P-PSDB; W59654.
XX Mouse cell surface antigen, 499E9 protein - used to treat conditions
PT associated with abnormal physiology or development
XX
XX Claim 4; Pages 8-11; 59pp; English.
XX
CC This is the nucleotide sequence encoding the mouse 499E9 protein, used
CC in the method of the invention to treat conditions associated with
CC abnormal physiology or development. The 499E9 protein is expressed
CC highly on polarised Th1 cells, binding of 499E9 to its receptor may
CC result in either immune cell expansion or apoptosis. Antagonists of
CC 499E9 may be used to modulate immune responses in abnormal situations,
CC e.g. autoimmune disorders including rheumatoid arthritis, systemic
CC lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well as
CC acute inflammatory responses in which T-cell expansion, activation or
CC immunological T-cell memory play an important role. The antibodies or
CC can be used to raise anti-idiotypic antibodies which will be useful
CC in detecting or diagnosing various immunological conditions related to
CC the expression of antigens of 499E9. The antibodies, and fragments of
CC 499E9 can be used in the treatment of conditions associated with
CC abnormal physiology or development, including abnormal proliferation
CC (e.g. cancerous conditions) or degenerative conditions.
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SQ Sequence 2191 BP; 605 A; 461 C; 518 G; 607 T; 0 other;

Query Match 100.0%; Score 2191; DB 19; Length 2191;
Best Local Similarity 100.0%; Prev. No. 0;
Matches 2191; Conservative 0; M.smatches 0; Indels 0; Gaps 0;

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RESULT	2					
V70284						
ID	V70284	standard; DNA: 2295 BP.				
XX	V70284;					
AC						
XX						
DT	11-FEB-1999	(first entry)				
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DE	Human osteoprotegerin binding protein encoding DNA from the 32D-F3 ins					
XX						
KW	Human; osteoprotegerin binding protein; OPG binding protein; arthritis					
KW	osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;					
KW	hypercalcaemia; osteoclast differentiation and activation receptor;					
KW	Payet's disease; ss.					
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OS	Homo sapiens.					
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PN	W09846751-Al.					
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PF	15-APR-1998; 98WO-US07584.					
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PR	16-APR-1997; 97US-0842842.					
PR	23-JUN-1997; 97US-0860855.					
XX						
PA	(AMGE-) AMGEN INC.					
XX						
PI	Boyle WJ;					
XX						
DR	WPI; 1998-594578/50.					
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DR	P-PSDB; W83194.					
XX						

PT Nucleic acid encoding osteoprotegerin binding protein - useful for,
 PT e.g. treating bone diseases by modulating osteoclast differentiation
 PT and for diagnosis
 PS
 PS
 XX Claim 1; Fig 1; 47pp; English.
 CC
 CC The present sequence encodes human osteoprotegerin (OPG) binding protein
 CC Host cells transfected with vectors containing nucleic acid molecules
 CC encoding OPG binding protein are used to produce recombinant OPG binding
 CC protein. OPG binding protein is used in binding assays to determine
 CC osteoprotegerin (OG) in biological samples; to screen for specific
 CC binding agents (particularly agonists and antagonists, including
 CC intracellular proteins); to raise Ab (useful in immunoassays for
 CC detection of OPG binding protein) and to identify compounds that
 CC modulate binding of OPG binding protein to osteoclast differentiation
 CC and activation receptor (OPAR). The nucleic acid molecule encoding OPG
 CC binding protein can be used to detect OPG binding protein-encoding
 CC sequences, e.g. screening for related sequences, also to produce
 CC transgenic animal models, while complementary sequences are used for
 CC antisense regulation of OPG binding protein expression. Modulators of
 CC OPG binding protein, particularly soluble forms of OPG binding protein
 CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
 CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
 CC disease, periodontal disease, osteoporosis, loosening of prostheses,
 CC optionally in combination with agents that promote bone growth.
 XX
 XX Sequence 2295 BP; 648 A; 487 C; 538 G; 622 T; 0 other;
 SS

	Query Match	97.94;	Score 2144..8;	DB 19;	Length 2295;		
	Best Local Similarity	99.4%;	Pred. No. 0;				
	Matches 2174;	Conservative	0;	Mismatches	12; Indels	2; Gaps	2;
Qy	1	GCCAGGACCTCTGTGAACCGTTCGGGGCGGGGGCCGCTGGCCGGAGTGCTGCTCGGCGG	60				
Dbb	34	gccdaggaacctctgtgaaccggttcgggggcggggcccgcttgcggggagtgctgtcgcgggg	93				
Qy	61	TGGGTGGCCGAGGAAGGAGAGAACGATTCGGCGAGCAGGGGCCCGCAACTCCGGCGCGCG	120				
Dbb	94	tgggtggcggaggaaaggagaacagatcgcggagcaggggcccgcgaactccggcgccg	153				
Qy	121	GCGCATGCGCGCGGCCAGCCGAGACTACGGCAAGTAGCTGCGCACGTGGCGACGTCGGAGGACATGGG	180				
Dbb	154	cgcatacgccggccggccagccagactacgccaagtacattgcgcagctcgaggaggatggg	213				
Qy	181	CAGCGGCCCGCGCGTCCCACACAGAGGGTCCCGTGCACCCCGCGCTTTGTGACCGGGCTCC	240				
Dbb	214	caggccccgggtcccaacagagggtccgctgcaccgcgccttgtgcacsgatcc	273				
Qy	241	GGCGCGGCACGCGCGCGCTCCGGTCCATGTTCTGTGGCCCTCTCTGGGGCTGGGACTGGG	300				
Dbb	274	ggcgcgcacccgcgcgctccgctccatgtctcgtggccctctcgtgggctgggactggg	333				
Qy	301	CCAGTGTGCTGCGACATCGCTCTCTTCTGTACTTTTCGAGCGCAGATGGATCCTTAACAG	360				
Dbb	334	ccaggtygtctgcagcatctgctctgttctgtacttttcgagcgcagatggaatccctaacag	393				
Qy	361	AATATCAGAAGACAGCACTCACTGCTTTTTATAGAACTCTGAGACTCCATGAAAACGCAGG	420				
Dbb	394	aatatcagaagacagcactcactgcttttatagaatectgagactccatgaaaacgcagg	453				
Qy	421	TTTGCAGGACTCGACTCTGGAGATGAGACACACTACTCTGACTCTCTGCAGGAGGATGAA	480				
Dbb	454	tttcaggactctgactctggagtggaagacactactgactctgtaggagatgaa	513				
Qy	481	ACAAGCCTTTTCAGGGGGCGGTGCAGAAAGAACTGCAACACATTTGTGGGGCCACAGCGCTT	540				
Dbb	514	acaagccttccaggggcccgltgagaaagaaactgcaaacacattgtggggccacagcgctt	573				
Qy	541	CTCAGGAGCTCCAGTATGATGGAAGGCTCATGTTTGGATGTGGCCCCACGAGCGCAAGCC	600				
Dbb	574	ctcaggagctccagctaTgatTggaaggtctatTggttgatTggtggccagcaggcaaTccc	633				

QY 601 TGAGGCCAGCCATTGTCACACCTCACCI.TCAATGCTGCCAGCATCCCATCGGTTCCCA 660
|||||
Db 634 tgaggccagccatttgcacacctccacc.tcaatgctgcgcagcatcccatcggttcccca 693
QY 661 TAAAGTCACTCTGCTCCCTTTGGTACCACIATCGAGGCTGGGCCAAGATCTCTAACATGAC 720
|||||
Db 694 taaagcaactctgctctcttggtaaccac.atcgaggctgggccaagatctctaacaatgac 753
QY 721 GTTAAAGCAACGGAAACTAAGGTTTAACTAAGATGGCTTCTATTACCTGTACGCCAACAT 780
|||||
Db 754 gtttaagcaacggaactaagggttaac.aagatggcttctattacctgtacgccaacat 813
QY 781 TTGCTTTGCGCATCATGAACATCGGGM.GCGTACCTACAGACTATCTTCACTGTATGGT 840
|||||
Db 814 ttgctttcggcatacgaacaatcgggat.gcgtaacctacagactatcttcagctgatggt 873
QY 841 GTATGCTGTTTAAACACGAGCATCAAAATCT.CAAGTCTTCATTAACCTGATGAAGGAGGAG 900
|||||
Db 874 gtaatgctgttaaaaccagcatcaaaatc.caagttctcataaactcgatgaagaggaggag 933
QY 901 CAGGAAAACTGCTCGGGCAATTTCTGAA.TCCACTTTTATTTCATTAATGTTGGGGGATT 960
|||||
Db 934 cagcaaaaactgctcgggcaattctgaaat.tccactttttatttcataaaatgttgggggatt 993
QY 961 TTTCAAGCTCCGAGCTGGTCAAGAAATTTGCATTCAGGTGTCACACCTTCCCTGCTGGA 1020
|||||
Db 994 ttccaagctccgagctgggtgaagaattt.gcattcagggtgccaacccctccctgctgga 1053
QY 1021 TCCGGATCAAGATGCGACGCTACTTTGGGCTTTTCAAGTTTCAGGACATAGACTCAGACTC 1080
|||||
Db 1054 tccggatcaagaatgcagcgtacttttgggcttttcagaagtttcaggacatagactgagactc 1113
QY 1081 ATTTCCGTGGAACATTAGCATGGATGTCCTC.AGATGTTTGGAAACTTCTTAAAAAATGGATG 1140
|||||
Db 1114 atttcgtgaacattagcatgatgctcctagatg.ttttggaaactctttaaanaatggatg 1173
QY 1141 ATGCTCTACATGTAAGACTACTAAGT.GACATGGCCACGGGTATGAACACTCACAGC 1200
|||||
Db 1174 atgtctatacatgtlaagactactaagtgacatg.gccaccggtgatgaactcacagc 1233
QY 1201 CPTCTCTTTGAGCCCTGACAGGTTGTGTATATGTAAGTCCATAGTGATGTTAGATTTC 1260
|||||
Db 1234 cctctctcttgagccctgtaagagttgtgtatata.tgtaaaatcccataggtgatgttagattc 1293
QY 1261 ATGGTGATTACACAACGGTTTACATTTTGTAAATGTTTCCTTAAGAAATTAACCCAGATT 1320
|||||
Db 1294 atggtattacacaacaggttttacaattttgtaagt.ttcct-agaattgaaaccagatt 1352
QY 1321 GGGAGAGGTATTCGGATGCTTATGA AAAA.CTTACAGTGGAGCTATGGAAGGGGTACAG 1380
|||||
Db 1353 gggagaggtattccgatgcttatagaaaaacttacacg.tgagctatggaagggggtcacag 1412
QY 1381 TCTCTGGGTCTAACCCCTGGACATGTCGCCACTGAGAACCTTGAAATTAAGAAATGCCAT 1440
|||||
Db 1413 tctctgggtcttaacccctggacatgtgcactgagaacaccttgaaattaaagagatgccat 1472
QY 1441 GTCATTTGCAAAAGAAATCATAGTGTGAAGGTTTAAAGTCTTTTCAATTTGTTACATTTGGCT 1500
|||||
Db 1473 gtcattgcaaaagaaaatgatagttgcagggttaagt.tctcttggaaatcgtaacattcgct 1532
QY 1501 GGGACCTGCAAAATAGTCTCTTTTCTTAAATGAGGAGAGAAAAATATATGATTTTATA 1560
|||||
Db 1533 gggacctgcaaaataagttctcttttctaatgagggagagaaaaatatgtattttata 1592
QY 1561 TAATGCTTAAAGTTATATTTTCAGGTGTAATGTTTCTGTCGCAAGTTTGTAAATATAT 1620
|||||
Db 1593 taatgtctaaagtataatttcaggttaagtgtttctctgtgcaaaagtttgttaaatataat 1652
QY 1621 TTGCTGTATAGTATTTGATTCAAAATATTFAAAAATGCTCTCACTGTGACATATTTAATG 1680
|||||
Db 1653 tctgcataagttattgatttcaaaaattcaaaaatgctcactgttgacatatttaagt 1712
QY 1681 TTTTAAATGTACAGATGTATTTAACTGGT.TCACTTTGTAATTCCTCCCTGAAAGGTACTCGTA 1740

Db 1713 ttttaaatgtacagatgatttaactggtgcactttgtaactttgtaattccctggaaggtactcgt 1772
QY 1741 GCTAAGGGGGCAGAAATACTGTTTCTGGTGCACACATGTAGTTTATTTCTTTATTTCTTTT 1800
|||||
Db 1773 gctaagggggcagaataactgtttctggtgcacacacatgtagttattcttcttcttctt 1832
QY 1801 AACTTAATAGAGTCTTCAGACTTGTCAAAACTATGCAAGCAAAATTAATAATAAAAAATA 1860
|||||
Db 1833 aacttaataagatcttcagactgtcacaactatgcaagcaaaaataaataaataaataa 1892
QY 1861 AATGAATATCTTCAATAATAAGTAGGTGTTGTCACACAGTGCTTTCAAATTTAGAA 1920
|||||
Db 1893 aatgaataaccttgaaataaataagtaggagttggtccaccaggtgctttcacaatttagaa 1952
QY 1921 GCTAATTTGACTTTAGGAGCTGACATAGCCAAAAAGGATACATAATAGGCTACTGAAAATC 1980
|||||
Db 1953 gctaattgacttttggagctgacatagccaaaaggatcacataataggtactg-aaatc 2011
QY 1981 TGTCAAGGAGTATTATGCAATTTATTGAACAGGTGCTTTTTCACAAAGAGCTACAAATG 2040
|||||
Db 2012 tgtcaggagttattatgcaattattgaacaggtgcttttttttacaagagctacaaaattg 2071
QY 2041 TAAATTTTGTCTCTTTTTCATAGAAATGTACTATATAGTTTATCAGCCAAAAAACA 2100
|||||
Db 2072 taaattttgtttctttttttcccatagaaaaatgtactatagttttatcagccaaaaaaca 2131
QY 2101 ATCCACATTTTAAATTTAGTGAAGCTTATTTTATTTATCTACTGTACATAAAGCATTTGTTTC 2160
|||||
Db 2132 atccactttttaaattagtgaaagttttttattattattactgtacaataaaagcattgtctc 2191
QY 2161 TGAATGGCATTTTGTGTTACTTTAAATAAT 2188
|||||
Db 2192 tgaatgtaatttttttggtaaaaaaat 2219

RESULT 3
299966
ID 299966 standard; DNA; 2299 BP.
XX 299966;
AC 299966;
XX
DT 25-JUL-2000 (first entry)
XX
DE DNA encoding a murine osteoprotegerin ligand (OPGL).
XX
KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
tumour necrosis factor receptor; type II transmembrane protein;
osteoclast differentiation; CSF-1; osteoclast activator;
immune response; osteoporosis; bone resorption; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 170..1120
FT /*tag= a
FT /product= "osteoprotegerin ligand"
XX
PN W0200015807-A1.
XX
PD 23-MAR-2000.
XX
PF 13-SEP-1999; 99WO-DK00481.
XX
PR 15-SEP-1998; 98DK-0001164.
PR 02-OCT-1998; 98US-0102896.
XX
PA (MEBI-) M & E BIOTECH AS.
XX
PI Halkier T, Haaning J;
XX
DR WPI; 2000-271444/23.
DR P-PSDB; Y84419.

XX In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
PT to treat, prevent and ameliorate osteoporosis -
XX
XX
PS Disclosure; Page 82-85; 110pp; English.
XX
XX The present sequence encodes a murine osteoprotegerin ligand (OPGL).
CC Osteoprotegerin is a secreted member of the tumour necrosis factor
CC receptor family, which blocks osteoclastogenesis in a dose dependent
CC manner. The OPGL protein is synthesised as a type II transmembrane
CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
CC is a potent osteoclast differentiation factor when combined with CSF-1.
CC It is not capable of inducing osteoclast differentiation in the absence
CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
CC specification describes a method for the in vivo down-regulation of
CC OPGL activity in an animal. The method comprises using at least one OPGL
CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
CC an immune response in the animal. The method and OPGL polypeptide are
CC useful for treating, preventing and ameliorating osteoporosis or other
CC diseases or conditions characterised by excessive bone resorption.
XX
XX Sequence 2299 BP; 641 A; 494 C; 541 G; 623 T; 0 other;
SQ

Query Match	97.98;	Score 2144.8;	DB 21;	Length 2299;
Best Local Similarity	99.4%;	Pred. No. 0;		
Matches 2174;	Conservative 0;	Mismatches 12;	Indels 2;	Gaps 2;

Qy	1	GCCAGGACCTCTGTGAACCGTCGGGGGGGGGGCGCGCTGTGCGGGAGTCTGCTCGGCGG	60
Db	46	gccaaggacctctgtgaaccggtctggagcggtggggcgcgctggcgggagtcgtctcgcgcg	105
Qy	61	TGGGTGGCCGAGGAAGGAGAGAACGATCGCGGAGCAGGGCCCGGAACCTCGGGCGCGCG	120
Db	106	tgggtggccgaaggaaggaagaaacgatcgcgagcaggcgcccgaaactccggcgccgcg	165
Qy	121	CGCCATGGCCGGCGGCCAGCCGAGACTACGGCAAGTACTTGCGCAGCTCGGAGGAGATGGG	180
Db	166	cgccatgcgcggcgccagcgagactacgcaagtacctgcgcagctcgaggagatggg	225
Qy	181	CAGCGGCCCGCGCTCCACACGAGGGTCGCTGCACCCCGCGGCTTCTGCACCGGCTCC	240
Db	226	cagcgcccgcgctcccaacacagggctccctgcaccccgcgctctgcacggctcc	285
Qy	241	GGCGCGCCACAGCCGCGCTCCCGCTCCATGTTCTTGGCCCTCTTGGGGCTGGGACTGGG	300
Db	286	ggcgcgccacccgcgcctcccgctccatgttctggccctctgggctcgtggagactggg	345
Qy	301	CCAGGTGTGTGCAGCATPGCTGTGTTCTGTACTTTGACGGCAGATPGGATPCTTAACAG	360
Db	346	ccagggtggtctgcagcatcgctctgtctgtacttttcgagcgagatggatccttaacag	405
Qy	361	AATATCAGAGACAGCACTCACTGCTTTATAGAAATCCTGAGACTCCATGAAACGCGAGG	420
Db	406	aatacagaagacagcactcactctttaaagaaatcctgagatcccatgaaacgcgag	465
Qy	421	TTTGCGAGACTCGACTCTGGAGAGTGAAGACACACTACTCTGACTCTCGAGGAGGATGAA	480
Db	466	tttgcaggactcgcactctggagagtgaagacacactaactgactctctgcaggagagatgaa	525
Qy	481	ACAAAGCCTTTTCAGGGGGCCGTCGAGAAGAACTGCAACACATGTTGGGGCCACAGCGGTT	540
Db	526	acaagcctttcagggggcggtgcagaaagaaactgcaacacatgtgggggccacagcgctt	585
Qy	541	CTCAGGAGCTCCAGTATGATGGGAAGGCTCATGTTGGATGTGGCCCGACGAGCGCAAGCC	600
Db	586	ctcaggagctccagctatgatgggaaggctcatgtgttgatgtggcccgagcgcaagcc	645
Qy	601	TGAGGGCCAGGCATTTGACACACTTCACCATCAATGCTGCCAGCATCCCATCGGTTCCCA	660
Db	646	tgaaggccagacaaattgcacacctcaacataaaagtcgcagcagcaccatcgggtctccca	705
Qy	661	TAAAGTCACCTGTGTCCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAACATGAC	720

[illegible]

Db 1785 gctaaagggggcagaataactgtttcttggtaccacatgtagttttatttcttcttatttcttctt 1844
QY 1801 AACCTTAATAGAGCTTCAGACTTGTCAAACTATGCAAGCAAAATAAATAAATAAATA 1860
Db 1845 aacttaataagagcttcagacttgtcaaatctatgaagcaaaataaataaataaataa 1904
QY 1861 AAATGAATATCTTGAATATAAAGTAGAGGTTGGTGCACCAAGGTGCCCTTTCAAATTTAGAA 1920
Db 1905 aaatgaataaccttgaaataataagtagaagtgttggtcaccaggtgcctcttcaaattagaa 1964
QY 1921 GCTAATGACTTTAGGAGCTGACATAGCCAAAAGGATACATAATAGGCTACTGAAATC 1980
Db 1965 gctaaatgactttgagcgtgacatagccaaaagaatacataataggctactg-aaatc 2023
QY 1981 TGTCAGAGTAGTATTATGCAATATTGAAAGAGTGCTTTTATACAGAGCTACAAATTC 2040
Db 2024 tgtcaggagtagttatgcaattattgaacaggtgtcttttttaccagagactacaaattg 2083
QY 2041 TAAATTTGTTCTTTTTCCTCATAGTAAATGTACTATAGTTTATCAGCCAAAANACA 2100
Db 2084 taaatttgtctcttttttcccccagaaaaatgtactatagttttatcagccaaaaaaca 2143
QY 2101 ATCCACTTTTAAATTTAGTGAAGTTATTTATTATACTGTACAATAAAGCAATTTGTTTC 2160
Db 2144 atccactttttaaattagtgaaagtattttattattattactgtacataaaaaagcattgtctc 2203
QY 2161 TGAATGGCATTTTTCGTACTTAAAAAT 2188
Db 2204 tgaatgttaatttttggtaaaaaaat 2231

RESULT 4

ID X80224 standard; cDNA; 2237 BP.
AC X80224;
XX
DT 17-AUG-1999 (first entry)
DE Murine TRANCE encoding cDNA.
XX
KW TRANCE: tumour necrosis factor superfamily; signal transduction; TNF;
KW TNF-related activation induced cytokine; immune response; cancer;
KW autoimmune disease; HIV; hypersensitivity; allergen; ds.
XX
OS Mus musculus.
XX
FH Key Location/Qualifier;
FT CDS 142..1092
FT /*tag= a
XX
XX WO9929865-A2.
XX
XX 17-JUN-1999.
XX
PF 14-DEC-1998; 98WO-US26486.
XX
PR 11-DEC-1998; 98US-0989479.
PR 12-DEC-1997; 97US-0989479.
PR 03-MAR-1996; 98US-0034099.
XX
PA (UYRQ) UNIV ROCKEFELLER.
XX
PI Choi Y, Josien R, Steinman R, Wn B;
XX
DR WPI; 1999-385609/32.
DR P-PSDB; Y1874.
XX
PT TNF like proteins for treating autoimmunity and cancer
XX
PS Claim 4; Fig 3; 164pp; English.
XX
CC The present sequence encodes murine TNF-related activation induced

CC cytokines (TRANCE). Human or murine TRANCE polypeptides or their
CC variants, fragments, derivatives or analogues may be used as modulators
CC of immune response in a mammal comprising, antisense sequences to
CC TRANCE and fusion proteins comprising human and/or murine TRANCE.
CC Agonists and antagonists of TRANCE, can be used to modulate immune
CC response by increasing or decreasing the life span of mature dendritic
CC cells and increasing or decreasing T cell activation. These techniques
CC are especially useful for treating immune system related conditions such
CC as HIV, cancer, autoimmune disease or hypersensitivity to an allergen.
CC The TRANCE polypeptides can be used to increase the viability of
CC dendritic cells in vivo or in vitro, especially when used in conjunction
CC with proteins of the tumour necrosis factor (TNF) superfamily (especially
CC CD40L or TNF-alpha).
XX
SQ Sequence 2237 BP; 636 A; 470 C; 519 G; 612 T; 0 other;

Query Match 93.5%; Score 2049.2; DB 20; Length 2237;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 2155; Conservative 0; Mismatches 23; Indels 12; Gaps 8;
QY 1 GCCAGGACCTCTGTGAACCGTCCGGGGGGGGCGCTGCGCGGGAGTCTGCTCGCGG 60
Db 22 gccaggacctttgtgaaccggtcgggggcggtggcgtggcgtggcgtggcgtggcgtgg 77
QY 61 TGGGTGCGCGAGGAGGAGAGACGATCGCGAGCAGCGCGCGCGCGCGCGCGCGCGCG 120
Db 78 tgggtgccccgagagagagagacgatcgcgagcagggcgccgagactccggcgcgcg 137
QY 121 CGCATCGCGCGCGCGCGCGAGACTACGGCAACTACTGCGCAGCTCGGAGGAGATGGG 180
Db 138 cgcatcgcgcgcgcgcgagactcggaagtaacctgcgactcgcgactcggaagatggg 197
QY 181 CAGCGCGCGCGCGCGTCCACACAGAGGTCGCTGCACCCCGCGCTTCTGACCGGCTCC 240
Db 198 cagcgccccggcggtccacacagagtcggctgcaccccgcgctctctgcacggctcc 257
QY 241 GCGCGCGCGCGCGCGCTCCCGCTCCATGTTCTTGGCCCTCTGGGGCTGGGACTGGG 300
Db 258 ggcgcgcgaacccgc 317
QY 301 CCAGGTGGTTCGAGCATCGCTCTGTTCTTCTGATCTTTCGAGCGCAGATGATCTTAACAG 360
Db 318 ccagggtggttcgagcatcgctctgttctgtacttttcgagcgcagatggtatcctaacag 377
QY 361 AATATCAGAAGACAGCAGCTACTGCTTTTATAGAACTCTGAGACTTCCATGAAACGCGAG 420
Db 378 aatatcagaagacagcactcactgcttttatagaaactcctgagactccatgaaaacgcagg 437
QY 421 TTTGCGAGACTCGACTCTGGAGAGTGAAGACACACTACCTGACTCTCTGCGAGGAGTCAA 480
Db 438 ttgagaggactcactctgagagtgagagacacactcactgactcctcgagaggatgaa 497
QY 481 ACAAGCCTTTTCAGGGGCGCGTGCAGAAAGAACTGCAACACATTTGTGGGGCCACAGCGCTT 540
Db 498 acaagccttttcagggggcgctgcagaagaaactgcaacacattgtggggccacagcgtt 557
QY 541 CTCAGGAGCTCCAGCTATGATGGAAGGCTCATGTTGGATGTGCCCGCAGCGAGCAAGCC 600
Db 558 ctcaaggagctccagctatgatggaaggctcatggttggatgtggccagcgagcaagcc 617
QY 601 TGAGGGCCAGCCATTTGCACACCTCACCATCAATGCTGCCAGCATCCCATCGGGTTCCCA 660
Db 618 tgaggccagccatttgacacacctcaccaatgctgacagcatcccatcggtttccca 677
QY 661 TAAAGTCACCTCTGCTCTTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTACATGAC 720
Db 678 taaagtcactcttctctcttggtaaccacgactcaggtggggccaagatctcttaacatgac 737
QY 721 GTTAAGCACAGGAAACTAAGGGTTAACCAAGATGGCTTCTATTACCTGTACGCCAACAT 780
Db 738 gtttaagcaacgaaaactaagggttaaccagaatggcttctattacctgtacgccaacat 797

QY 781 TTGCTTTTCGGCATCATGAAACATCGGGAAGCGTACCTACAGACTATCTTCAGCTGATGGT 840
|||||
Db 798 tgccttttcggcatcatgaacaatcgggaagcgtaccacagactatcttcagctgaaggt 857
|||||
QY 841 GTATGCTGTTAAACACGAGCATCAAAATCCCAAGTTCTCATAACTGATGAAGAGGGAG 900
|||||
Db 858 gtatgctgttaaaaccagcatcaaaatcccaagttctcataaactgatgaagaagaggaag 917
|||||
QY 901 CACGAAAACTGTGCGGGCAATTCCTGAATTCACATTTTATTCCTAATAATGTGGGGGAT 960
|||||
Db 918 cacgaaaaactggtcgggcaatcttgaattccacttttattccataaagtgtgggggatt 977
|||||
QY 961 TTTCAAGCTCCGAGCTGCTCAAGAAATAGCATTCAGTGTCCCAACCTTCCTCCCTCGGA 1020
|||||
Db 978 ttccaagctccgagctggtggaagaaatagcattcaggtgtcccaacctctccctgctgga 1037
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QY 1021 TCCGGATCAAGATGCGACGTACTTTGGGGCTTTCAAAAGTTTCAGACATAGACTGAGACTC 1080
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Db 1038 tccggtacaagatgcgacgtactttggggcttcaaaagttcaggacatagactgagactc 1097
|||||
QY 1081 ATTCGTGGAAACATTAGCATGGATGCTCTAGATGTTTGGAAACTTCTTAAAAATGGATG 1140
|||||
Db 1098 atttcgtggaacattagcatggtctctagatgttgcgaactcttataaaatggatg 1157
|||||
QY 1141 ATGCTCTACATGTGAAGACTACTTAAGACACATGCGCCACGGGTGTATGAACATCACAGC 1200
|||||
Db 1158 atgctatacatgtlaagactactaagacatgcccacgggtgatgaacctcacagc 1217
|||||
QY 1201 CCFCTCTCTTGAG-CCTGTACAGTCTGTATATGTAAGTCCATAGTAGTGATGTAGATT 1259
|||||
Db 1218 cctctctctgagccctgtcacaggtctgctatcgtctaaagttcccataggtgctagatt 1277
|||||
QY 1260 CATGGTGATTACAAACGGTTTACAAATTTGTAATGATTTCCTAAGAATTGAACCCAGAT 1319
|||||
Db 1278 catggtgattacacaacggtttacaattttgtaagtattcct-agaattgaaccagat 1336
|||||
QY 1320 TGGGAGAGGTATTCGATGCTTATGAANAACTTACACGTGAGCTATGGAAGGGGGTCACA 1379
|||||
Db 1337 tgggagaggtattcccatgcttatgaaaaacttacacgtgagctatggaagggggtcac 1396
|||||
QY 1380 GTCTCTGGGTCTAACCCCTGGACATGTGCCACTGAGAACCTTGAATTAAGAACATGCCA 1439
|||||
Db 1397 gtctct-ggtctaacctctggacatgtgccactgagaaaccttgaaattaagagagatgcc 1455
|||||
QY 1440 TGTCATTGCAAGAAATGATGATGTGAAGGGTTAAGTTCCTTTTGAATTTGATACATTCGC 1499
|||||
Db 1456 tgcattgcatagaaatgatlgtgaagggttaagttcttcttgaaattgttacattgcgc 1515
|||||
QY 1500 TGGGACCTGCAAAATAGTCTCTTTTTCCTAATGAGGAGAGAAAATATATGATTTTAT 1559
|||||
Db 1516 tgggacctgcaataaagtctcttttcttaagtgcg--gagaaaaatatagtatttttat 1573
|||||
QY 1560 ATAATGCTAAAGTTATATTTCAGGTGATGTTTCTGTGCAAGTTTGTAAATTTATA 1619
|||||
Db 1574 ataagtctaaagtataatttcagggtgaatgtttctgtgcgaagtttgcgaattata 1633
|||||
QY 1620 TTTGTGCTATAGTATTGATTCAAAATATTTAAAAATGCTCACTGTTGCATATTTAAAT 1679
|||||
Db 1634 ttgtgctataglatttgattcaaaaatatttaaaaaatgtctcactgttgacataattta 1693
|||||
QY 1680 GTTTTAAATGTACAGATGATTTTAACTGGTGCACCTTTTGTAAATCCCTGGAAGGTACTCGT 1739
|||||
Db 1694 gttttaaaatgacagatgatttaacttgcacttgcacttgcacttgcacttgcacttgcact 1753
|||||
QY 1740 AGCTAGGGGGAGATGATGTTTCTGGGTGACCAACATGTAGTTTATTTCTTTTCTTTT 1799
|||||
Db 1754 agctaggggggcagaatactgttctgtgtgaccacatgtagtattcttcttcttctt 1813
|||||
QY 1800 TAACTTAATAGACTCTTCACATGTGTCAAACTATGCAAGCAAAATATAAATAAATAAAT 1859
|||||
Db 1814 taacttaatagactcttcagactgttcaaaactatgcaagcaaaaataaaataaaataaa 1873
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QY 1860 AAAATGAATATCTTGAATAATAAGTAGGATGTTGGTCACCAGGTGCCTTTTCAAAATTTAGA 1919
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Db 1874 aaaaagaaacccttgaaataagtaggtgttggccaccaggctctttccaatttaga 1933
|||||
QY 1920 AGCTAATTCAGCTTTAGGAGCTGACATAGCCAAAAGGATACATAATAGGCTACTGAAAAT 1979
|||||
Db 1934 agctaattgacttttaggagctgacatagccaaaagga-acataataggctactg-aaat 1991
|||||
QY 1980 CTGTCAGAGAGTATTTATGCAATTTATGACAGGTGCTCTTTTTCACAGAGCTACAAAT 2039
|||||
Db 1992 ctgtcaggagatttcatgcaattattgacaggtgcttttttttacaagagctacaaatt 2051
|||||
QY 2040 GTAAATTTT-GPTTCTTTTTCATAGCAATTTTCCCATAGAAAATCTACTATATGATATATCAGCCAAAAA 2098
|||||
Db 2052 gtaaatcttggtctctctctctctctcccatagaaaatgtactatagtttaccagccaaaaa 2111
|||||
QY 2099 CAATCCACTTTTAAATTTAGTGAAGTTATTTATTTATCTGTACAAATAAAGCATTGTT 2158
|||||
Db 2112 caatccactttttaaatttagtgaagttattttattattactgtacataaaaagcattgct 2171
|||||
QY 2159 TCTGAATGGCATTTTGTGCTACTTAAAAAT 2188
|||||
Db 2172 tctgaatgttaatttttgggtacaaaaat 2201
|||||
RESULT 5
V41377
ID V41377 standard; cdna; 1630 BP.
XX
AC V41377;
XX
DT 08-OCT-1998 (first entry)
XX
DE NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
XX
KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW immune response; inflammatory response; toxic shock; sepsis;
KW RANKL; RANK ligand; tumour necrosis factor; TNF; mouse; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 3..887
FT /*tag= a
FT /product= "murine RANKL (ligand for RANK)"
XX
PN WO9828426-A2.
XX
PD 02-JUL-1998.
XX
XX 22-DEC-1997; 97WO-US23775.
PF
PR 14-OCT-1997; 97US-0064671.
PR 23-DEC-1996; 96US-0059978.
PR 07-MAR-1997; 97US-0813509.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Anderson DM, Galibert LJ, Maraskovsky E;
XX
DR WPI; 1998-377657/32.
DR P-PSDB; W69956.
XX
PT New isolated ligand for receptor activator of NF-kappa B - used to
PT develop products for augmenting an immune response for inhibiting an
PT inflammatory response and for protection of cells
XX
PS Claim 25; Pages 55-57; 80pp; English.
XX
CC This cDNA encodes a murine RANKL, a ligand for the RANK (receptor
CC activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a
CC member of the tumour necrosis factor (TNF) family. A soluble RANK
CC may be used for inhibiting activation of NF-kB, by contacting a cell
CC expressing membrane-associated RANK with a soluble RANK which binds to

RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used to induce maturation of dendritic cells and enhance their allo-stimulatory capacity, thereby augmenting an immune response. The soluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF- κ B by RANK antagonists may be useful in ameliorating negative effects of an inflammatory response that result from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host reactions, or acute inflammatory reactions. They can also be used as adjunct therapy for disease characterised by neoplastic cells that express RANK. RANKL polypeptides can also be used to identify inhibitors of RANK and thus inhibitors of an inflammatory response, and also for protecting RANK-expressing cells from the negative effects of chemotherapy or the presence of high levels of TNF- α . The products can also be used for detection and drug screening.

XX Sequence 1630 BP; 436 A; 355 C; 379 G; 460 T; 0 other;

Query Match 73.7%; Score: 1615.8; DB 19; Length 1630;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1628; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 189 CCGCGCTCCACAGGAGGTCGCAACCGCGCTCTGACCGGCTCCGCGCGCGC 248
DB 1 CCGCGCTCCACAGGAGGTCGCAACCGCGCTCTGACCGGCTCCGCGCGCGC 60

QY 249 CACCGCGCGCTCCGCTCCATGTTCTCTGCGCTCCGCGGCTGGGCTGGGCTGGG 308
DB 61 CACCGCGCGCTCCGCTCCATGTTCTCTGCGCTCCGCGGCTGGGCTGGGCTGGG 120

QY 309 TCTGACGATCGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 368
DB 121 TCTGACGATCGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180

QY 369 AACACAGCACTCACTGCTTTTAGAATCTGAGACTCCATGAAACGAGGTTTGCGG 428
DB 181 AAGACGACCTCACTGCTTTTAGAATCTGAGACTCCATGAAACGAGGTTTGCGG 240

QY 429 ACTGCTGCTGAGAGTGAAGACACACTCTCTGACTCTCGACGAGGATGAACAGCCT 488
DB 241 ACTGCTGCTGAGAGTGAAGACACACTCTCTGACTCTCGACGAGGATGAACAGCCT 300

QY 489 TTCAGGGGGCGCTGCAGAAAGAACTGCA/CACATTTGCGGGCCACACGCGCTTCTCAGGAG 548
DB 301 TTCAGGGGGCGCTGCAGAAAGAACTGCA/CACATTTGCGGGCCACACGCGCTTCTCAGGAG 360

QY 549 CTCGAGTATGATGGAAGGCTCATGGTTGATGTGGCCCGACGAGGCAACGCTGAGGCC 608
DB 361 CTCGAGTATGATGGAAGGCTCATGGTTGATGTGGCCCGACGAGGCAACGCTGAGGCC 420

QY 609 AGCCATTGTCACACCTCACCATCAATGCTGCCAGCATCCCATCGGTTCCCATAAAGTCA 668
DB 421 AGCCATTGTCACACCTCACCATCAATGCTGCCAGCATCCCATCGGTTCCCATAAAGTCA 480

QY 669 CTCTGCTCTTGGTACCAGATCGAGGCTGGGCCAAGATCTCTAACATCAGCTTAAGCA 728
DB 481 CTCTGCTCTTGGTACCAGATCGAGGCTGGGCCAAGATCTCTAACATCAGCTTAAGCA 540

QY 729 ACGGAAACTAAGGGTTAACCAAGATGGCTTCATTATACCTGTACGCCAACATTTGCTTC 788
DB 541 ACGGAAACTAAGGGTTAACCAAGATGGCTTCATTATACCTGTACGCCAACATTTGCTTC 600

QY 789 GGCATCATGAACATCGGAGGCTACCTACACACTATCTTCAGCTGATGCTATGCTG 848
DB 601 GGCATCATGAACATCGGAGGCTACCTACACACTATCTTCAGCTGATGCTATGCTG 660

QY 849 TTAACACACGATCAAAATCCCAAGTTCTCATAACTGTAGAAAGGAGGAGGACGACGAAA 908
DB 661 TTAACACACGATCAAAATCCCAAGTTCTCATAACTGTAGAAAGGAGGAGGACGACGAAA 720

QY 909 ACTGGTGGGCAATCTGAATCCACTTATTTCCATTAATTTGGGGGATTTTTCAGC 968
DB 909 ACTGGTGGGCAATCTGAATCCACTTATTTCCATTAATTTGGGGGATTTTTCAGC 968

DB 721 ACTGCTGGGCAATCTGAAATCCACTTTTATCCATAAATGTTGGGGATTTTCAAGC 780

QY 969 TCCGAGCTGGTGAAGAAATTAGCAATTCAGGTGTCCCAACCTTCCCTGCTGGATCCGGATC 1028

DB 781 TCCGAGCTGGTGAAGAAATTAGCAATTCAGGTGTCCCAACCTTCCCTGCTGGATCCGGATC 840

QY 1029 AAGATGGACACTACTTTGGGGCTTTTCAAGTTCAGGACATAGACTGAGACTCATTTTCG 1088

DB 841 AAGATGGACACTACTTTGGGGCTTTTCAAGTTCAGGACATAGACTGAGACTCATTTTCG 900

QY 1089 GAACATTAGCATGATGCTTCTAGATGTTGGAAACTTCTTAAAAATGCATGATCTAT 1148

DB 901 GAACATTAGCATGATGCTTCTAGATGTTGGAAACTTCTTAAAAATGCATGATCTAT 960

QY 1149 ACATGTGTAAAGACTACTAAGAGACATGCCACGCTGTATGAACCTCACAGCCCTCTCTC 1208

DB 961 ACATGTGTAAAGACTACTAAGAGACATGCCACGCTGTATGAACCTCACAGCCCTCTCTC 1020

QY 1209 TTGAGCCCTGTACAGGTTGCTATATGTAAAGTCCATAGGTGATGTAGATTGATGCTGAT 1268

DB 1021 TTGAGCCCTGTACAGGTTGCTATATGTAAAGTCCATAGGTGATGTAGATTGATGCTGAT 1080

QY 1269 TACACACGGTTTACAAATTTTGTAAATGATTTCTTAAAGATGAACACAGATTGGAGAGG 1328

DB 1081 TACACACGGTTTACAAATTTTGTAAATGATTTTCTTAAAGATGAACACAGATTGGAGAGG 1139

QY 1329 TATTCCGATGCTTATGAAGAACTTACACGTGAGCTATGAAAGGGGTGACAGCTCTCTGG 1388

DB 1140 TATTCCGATGCTTATGAAGAACTTACACGTGAGCTATGAAAGGGGTGACAGCTCTCTGG 1199

QY 1389 TCTAACCCCTGGACATGTCACACTTCAGAACCTTGAAGATTAAGAAATGCAATGCTATTC 1448

DB 1200 TCTAACCCCTGGACATGTCACACTTCAGAACCTTGAAGATTAAGAAATGCAATGCTATTC 1259

QY 1449 AAAGAAATGATAGTGTGAAGGTTAAGTCTTTTGAATTTGTACATTCGCTGGACCTG 1508

DB 1260 AAAGAAATGATAGTGTGAAGGTTAAGTCTTTTGAATTTGTACATTCGCTGGACCTG 1319

QY 1509 CAATAAGTCTCTTTTCTTAATGAGGAGAGAAATAATATATGATTTTATATATATGCT 1568

DB 1320 CAATAAGTCTCTTTTCTTAATGAGGAGAGAAATAATATATGATTTTATATATATGCT 1379

QY 1569 AAAGTATATTTACAGTGTAAATGTTTCTGTGCAAGTTTGTAAATTTATTTTCTGCTA 1628

DB 1380 AAAGTATATTTACAGTGTAAATGTTTCTGTGCAAGTTTGTAAATTTATTTTCTGCTA 1439

QY 1629 TAGTATTTGATTTCAAAATATTTAAATAATGCTCTGCTGACATATTTAAATGTTTAAAT 1688

DB 1440 TAGTATTTGATTTCAAAATATTTAAATAATGCTCTGCTGACATATTTAAATGTTTAAAT 1499

QY 1689 GTACAGATGATTTTAACTGGTGCACCTTTGTAATTTCCCTGAGGTACTCGTAGCTAAGGG 1748

DB 1500 GTACAGATGATTTTAACTGGTGCACCTTTGTAATTTCCCTGAGGTACTCGTAGCTAAGGG 1559

QY 1749 GGCAGATACGTTTCTGCTGACACCATGATGTTTATTTTCTTTTATTTTCTTTTAACTTAAT 1808

DB 1560 GGCAGATACGTTTCTGCTGACACCATGATGTTTATTTTCTTTTATTTTCTTTTAACTTAAT 1619

QY 1809 AGAGTCTTCAG 1819

DB 1620 AGAGTCTTCAG 1630

RESULT 6

V41371

ID V41371 standard; cDNA; 1630 BP.

XX

AC V41371;

XX

DT 08-OCT-1998 (first entry)

XX

DE NF- κ B receptor activator RANK ligand (RANKL) encoding cDNA.

XX

KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 KW immune response; inflammatory response; toxic shock; sepsis;
 KW RANKL; RANK ligand; tumour necrosis factor; TNF; mouse; ss.

OS Mus musculus.

Key Location/Qualifiers
 CDS 3..887
 FT /*tag= a
 FT /product= "murine RANKL (ligand for RANK)"

PN WO9828424-A2.

PD 02-JUL-1998.

PP 22-DEC-1997; 97WO-US23866.

PR 14-OCT-1997; 97US-0064671.

PR 23-DEC-1996; 96US-0059978.

PR 07-MAR-1997; 97US-0813509.

XX (IMMUNEX) IMMUNEX CORP.

XX Anderson DM, Galibert LJ, Maraskovsky E;

XX WPI; 1998-377655/32.

XX P-PSDB; W68292.

XX New isolated receptor activator of necrosis factor-kappa B - useful

XX for, e.g. developing products for regulating an immune or

XX inflammatory response, treating toxic shock or sepsis

XX Example 7; Pages 55-57; 80pp; English.

XX This cDNA encodes a murine RANKL, a ligand for the RANK (receptor

XX activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a

XX member of the tumour necrosis factor (TNF) family. Host cells transformed

XX or transfected with an expression vector comprising the RANK encoding

XX nucleic acid can be used to produce recombinant RANK protein. The soluble

XX RANK may be used for inhibiting activation of NF-kB, by contacting a cell

XX expressing membrane-associated RANK with a soluble RANK which binds to

XX RANK ligand (RANKL). The soluble RANK polypeptide composition may also be

XX used for regulating an immune or inflammatory response. Inhibition of

XX NF-kB by RANK antagonists may be useful in ameliorating negative effects

XX of an inflammatory response that result from triggering of RANK, e.g. in

XX treating toxic shock or sepsis, graft-versus-host reactions, or acute

XX inflammatory reactions. They can also be used in adjunct therapy for

XX disease characterised by neoplastic cells that express RANK. The products

XX can also be used for detection and drug screening.

XX Sequence 1630 BP; 436 A; 355 C; 379 G; 460 T; 0 other;

XX

XX Query Match 73.7%; Score 1615.8; DB 19; Length 1630;

XX Best Local Similarity 99.8%; Pred. No. 0;

XX Matches 1628; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

XX

QY 429 ACTCGACTCTGGAGAGTGAAGCAACACACACTACCTGACTCTCTGCAGGAGGATGAACACAGCCT 488
 DB 241 accgactctggagagtgaagacacacactacactgactctcctgagggagatgaacaagct 300
 QY 489 TTCAGGGGGCGTGCAGAGAAGCAACTGCAACACATTTGTGGGCCACAGCGCTTCTCAGGAG 548
 DB 301 ttcagggggcggtgcagagaagaactgaacacattgtg99ggccacagc9cttctcagagag 360
 QY 549 CTCAGCTATGATGAAGAGGCTCATGTGTGGATGTGGCCCGCCAGCGAGGAGCCTTGAGGCC 608
 DB 361 ctccagctatgatgaaggtcatgttggatgtg99cccgagcgagcctgagggccc 420
 QY 609 AGCCATTTGACACACCTCACCATCAATGCTGCCAGCATCCCATCGGGTTCCTCAATGAATCA 668
 DB 421 agccatttgacacctcaccatcaatgtgcagcagcatcccatcggttcccaaaagtca 480
 QY 669 CTCTGTCTCTTGGTACACGATCGAGCTGGGCCAAGATCTCTAACATGAGCTTAAGCA 728
 DB 481 ctctgtctcttgggtaccacgagatcgaggtg99ccaaagatctctaacatgacgttcaagca 540
 QY 729 ACGAAAACTAAGGGTTAACCAAGATGCTTCTATTACTCTGTACGCCCAACATTTGCTTTC 788
 DB 541 acgaaaaactaagggttaaccaagatggtctctattacctgtacgcaacattgtcttc 600
 QY 789 GGCATCATGAACATCGGGGAAGCGTACTACAGACTATCTTCAGCTGATGTGTATGTCG 848
 DB 601 ggcattcatgaacatcggggaagcgtacctacagactatcttcagctgattgtgtatgtcg 660
 QY 849 TTAACACACATCAAAATCCCAAGTTCTCATACCTGATGAAGGAGGAGGACGACGAAA 908
 DB 661 ttaaacaccagcatcaaaatcccaagttctcataaccctgatgaaagggagggagcagcaaa 720
 QY 909 ACTGGTCGGGCAATTCCTGAATTCACACTTTTATCCATAAATTTTGGGGGATTTTTCAGAC 968
 DB 721 actggtcgggcaattctgaattcccaatttattccataaatgttgggggatttttcaagc 780
 QY 969 TCGAGCTGTGGAAGAAATAGCATTCAGGTGTCCAACCTTCCCTGCTGTGATCGGATC 1028
 DB 781 tcgagctgtggaagaaatagcattcagggtgtccaaaccttccctgctggatccggatc 840
 QY 1029 AAGTGGAGCTACTTTGGGGCTTTCAAAGTTCAGGACATAGACATGACATCATTTTCGTG 1088
 DB 841 aagatgcagctacttctggggcttccaagttcaggacatagactgagactcattctgtg 900
 QY 1089 GAACATTAGCATGATGCTCTAGATGTTGAAACTTCTTAAAAATGGATGATGCTAT 1148
 DB 901 gaacattagcatggatgctctagatgttggaaacttcttaaaaaatggatgattcttat 960
 QY 1149 ACATGTTAAGACTACTAAGAGACATGGCCCGCCAGGTGTATGAACCTACAGCCCTCTCTC 1208
 DB 961 acatgtgtaagactactaagagacatggcccgctgtatgaaactcacagccctctctc 1020
 QY 1209 TTGAGCCTGTACAGGTTGTATATGTAATGTAAGTTCATAGGTGATTTAGATTCATGCTGAT 1268
 DB 1021 ttgagcctgtacaggttgtgtatatgtaagtcctcattaggtgattgattcattcgtgat 1080
 QY 1269 TACACAAACGGTTTACAAATTTTGAATTTCTTCTAAGAAATGAACACAGATTGGGAGAGG 1328
 DB 1081 tacacaacgggttttacaatttttgaatttctcaatgatttctct - agaatgtaaceagattggagaggg 1139
 QY 1329 TATTCGATGCTTATGAAAAAATTTACAGTGTAGCTATGGAAGGGGGTGCACAGTCTCTCGG 1388
 DB 1140 tattcagctgtcttatgaaaaacttacacgtgagctatggaagggggttcacagctctctggg 1199
 QY 1389 TCTAACCCCTGGACATGTCGACATGAGAACCTTGAATTTAAGAAATTAAGAAATGCCATGTCATTCG 1448
 DB 1200 tctaaaccttgacatgtgccactgagaaccttgaattgaagagagatgccatgcatcgtc 1259
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 QY 1509 CAAATAAGTTCTTTTTTCTTAATGAGGAGAAAAATATATGTAATTTTATATATATGCT 1568

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Qy	841	GTATGTCGTTAAACCCAGCATCAAAATCCCAAGTTCTCTATAACCTGATGAAGAGGGAG	900
Db	841	gtatgctgttaaaaccagcatcaaaatcccaagttctcataacctgatgaagagaggag	900
Qy	901	CACGAAACCTGGTCGGCAATTCTGAATTCACACTTTTATTCACATAAATGTTGGGGATT	960
Db	901	cacgaaaactggtcgggcaattctgaattccacttttatccataaattgttggggatt	960
Qy	961	TTTCAAGCTCCGAGCTGGTGAAGAATAAGCATTCAGGTGTCACACCCCTCCCTGCTGGA	1020
Db	961	tttcaagctcccgagctggtggaagaaattagcatctcaggtgtccaaaccttccctgctgga	1020
Qy	1021	TCCGATCAAGATCGCAGCTACTTTGGGCTTTCAAGTTTCAGGACATAGACTGAGACTC	1080
Db	1021	lccggatcaagatgcgacgtactttgggctttccaaagttcaggacatagactgagactc	1080
Qy	1081	ATTTCTGGACATTTAGCATGGATGTCCTAGATGTTTGGAACTTCTTAAAAATGGATG	1140
Db	1081	atttcgtggaacattagcatggatgctcctagatggtttggaaacttctaaaaaatggatg	1140
Qy	1141	ATGCTATACATGCTTAAGACTACTAAAGACATGCCCCACGGTGATGAACTCACAGC	1200
Db	1141	atgtctatcacatgtgcaagactactaaagacatgcccacggtgcatgaaactcacagc	1200
Qy	1201	CCTCTCTTTGAGCCTGTACAGGTTCTGTATATGTAAAGTCCATAGGTGATGTAGATT	1260
Db	1201	cctctcttgagcctgtacaggttgttatatgtaagttccatagtgatgtagattc	1260
Qy	1261	ATGGTGATTACACACGGTTTACAAATTTTGTAAATGATTTCTTAAGAAATGAACCA	1320
Db	1261	atggtgattacacaacggttttacaaattttglaatttccct-agaattgaaccagatt	1319
Qy	1321	GGGAGAGCTATTCCGATGCTTATGAAAACTTACACGTGAGCTATGGAAGGGGTCACAG	1380
Db	1320	gggagaggtatctccgatgctctatgaaaactcacagtgagctatggagggggtcacag	1379
Qy	1381	TCTCTGGCTCTAACCCCTGGACATGGCCACTTGAGAACCTTGAATTAAGAGATGCCAT	1440
Db	1380	tctctgggtctaaacccctggacatgcccactgagaaccttgaaattgaagagatgccat	1439
Qy	1441	GTCATTGCAACAGAAATGATAGTGTGAAGGTTAAAGTTCTTTTGAATTTACATTTGG	1500
Db	1440	gtcattgcaagaaatgatagtgtaaggggttaagtctcttttgaattgttacattgcgt	1499
Qy	1501	GGGACCTGCAATATAGTTCTTTTCTTAANTCAGGAGAG	1539
Db	1500	gggacctgcaaatagttcttttttcttaatgaggag	1538
RESULT 8			
Z99964			
ID	Z99964	standard; DNA; 2271 BP.	
XX	XX		
AC	AC		
XX	Z99964;		
XX	XX		
DT	25-JUL-2000	(first entry)	
XX	XX		
DE	DNA encoding a human osteoprotegerin ligand (OPGL).		
XX	XX		
KW	Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;		
KW	tumor necrosis factor receptor; type II transmembrane protein;		
KW	osteoclast differentiation; CSF-1; osteoclast activator;		
KW	immune response; osteoporosis; bone resorption; ss.		
XX	XX		
OS	Homo sapiens.		
XX	XX		
FI	Key	Location/Qualifiers	
FT	CDS	185..1138	
FT	FT	/*tag= a	
FT	FT	/product= "osteoprotegerin ligand"	
XX	XX		

PN	WO200015807-A1.	
XX		
PD	23-MAR-2000.	
XX		
PF	13-SEP-1999; 99WO-DK00481.	
XX		
XX	15-SEP-1998; 98DK-0001164.	
PR	02-OCT-1998; 98US-0102896.	
XX		
XX	(MEBI-) M & E BIOTECH AS.	
PA		
XX		
PI	Halkier T, Haaning J;	
XX		
DR	WPI; 2000-271444/23.	
DR	P-PSDB; Y84417.	
XX		
PT	In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used	
PT	to treat, prevent and ameliorate osteoporosis -	
XX		
PS	Disclosure; Page 75-77; 110pp; English.	
XX		
CC	The present sequence encodes a human osteoprotegerin ligand (OPGL).	
CC	Osteoprotegerin is a secreted member of the tumour necrosis factor	
CC	receptor family, which blocks osteoclastogenesis in a dose dependent	
CC	manner. The OPGL protein is synthesised as a type II transmembrane	
CC	protein. The murine and human OPGL polypeptides are 87% homologous. Op	
CC	is a potent osteoclast differentiation factor when combined with CSF-1	
CC	It is not capable of inducing osteoclast differentiation in the absence	
CC	of CSF-1. OPGL is also an activator of mature osteoclasts. The	
CC	specification describes a method for the in vivo down-regulation of	
CC	OPGL activity in an animal. The method comprises using at least one OP	
CC	polypeptide or subsequence, and/or at least one OPGL analogue to induc	
CC	an immune response in the animal. The method and OPGL polypeptide are	
CC	useful for treating, preventing and ameliorating osteoporosis or other	
CC	diseases or conditions characterised by excessive bone resorption.	
XX		
XX	Sequence 2271 BP: 658 A: 452 C: 522 G: 629 T: 0 other:	

Query Match	51.18;	Score 1118.8;	DB 21;	Length 2271;
Best Local Similarity	76.3%;	Pred. No. 3.7e-253;		
Matches 1659;	Conservative 0;	Mismatches 437;	Indels 78;	Gaps 20;
QY	36	GCCTGGCGGGAGTCTGCTCGCGCGTGGGTGGCGAGGAGGAGGAGACGATCGCGGAG	95	
Db	94	ggctccgcgcagcctccgcgaattggccgcagacaaagagggagggagcgagggagggga	153	
QY	96	CAGGCGCGCCGAACTCCGGGGCGCC--GGCCCATGTCGCGCGGCCAGCCGAGACTACGGCAA	153	
Db	154	ggagagctccgaagcgagagggccgcgcgcctatgcgcgcgcagacagactacaccaa	213	
QY	154	GTACTCTGGCAGCTCGGAGGAGATGGGAGCGGCGCCCGGCTCCACACGAGGGTCCGCT	213	
Db	214	gtacctcgtgctcgcgagggatggggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	273	
QY	214	GCACCGCGCGCTTCTGCACCGGCTCGCGCGCGCCACCGCGCGCTCCGCTCCATGTT	273	
Db	274	gcacgcgccgcg---cgcgcctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc	330	
QY	274	CCTGGCGCTCTCGGGGCTGGGACTCGGCGCAGGTGGTCTGCGACATCGCTCTGTCCTGTA	333	
Db	331	cgtgcccctcctgggctggggctggggcaggttgtctgcagctgcgcctgtttctta	390	
QY	334	CTTTGAGCGCGAGTGGATCTACAGAAATACAGACAGACACTACTGCTTTTATAG	393	
Db	391	tttcagagcgcagatggatccatagaatacagaagatggcactcactgcatttatag	450	
QY	394	AATCCTCGAGCTCCATGAAACGCGAGTTTTCGAGGACTCGACTGCGAGAGTGAAGACAC	453	
Db	451	aatttgagactccatgaaatgcagattttcagacacaaactctggagatccaagatcac	510	
QY	454	-----ACTACCTTCACATCTCGAGGAGATCAACAAAGCTTTTCAGGGGGCGCTCGAAC	507	

Db 511 aaattaatcacctgattcatgtaggagaa:taaacagggcctttcaggagcgtgtgcacaaa 570
Qy 508 GGAACGTGAACACTGTTGGGGCCACAGG:CTTCTCAGGAGCTCCAGCTATCATGATGGAAGG 567
Db 571 ggaattacaacatacgtttggatcacag:caatcacagagcagagaagcgtgtggtgag 630
Qy 568 CTCATGTTGGATGTGGCCACGACGAGGCA:GCTTGGAGGCCACGCCATTGTGCACACTCAC 627
Db 631 ctcaegggttagatctggccaagaggagca:gccttgaagctcagccttttgcctcatctcac 690
Qy 628 CATCAATGCTGCCACGATCCCATCGGGTTC:CCATAAAGTCACTCTGCTCTTTGGTACCA 687
Db 691 tattaatgccccagacatcccatctcgtgtt:ccataaagtgagctgcctcttgggtacca 750
Qy 688 CCATCGAGGCTGGGCCAAGATCTCTAAACATGACGT:TAAGCAACGGAACAACTAAGGGTTAA 747
Db 751 tgatcggggttgggccaagatctccaaca:gacttttagcaatggaaaactaatagttaa 810
Qy 748 CCAAGATGGCTCTTATACCTGTAGCCCA:CATTTGCTTTCCGGCATCATGAACATCGGG 807
Db 811 tcaggatggctttattaccctgtatgcga:caatttgccttcgacatcatgaaccttcagg 870
Qy 808 AAGCGTACCTACAGACTATCTCAGCTGA:GGTGTATGCTCTTAAACAGCATCAAAAT 867
Db 871 agaccctagctacagagtatcttccaactaa:gggtacgtcactaaaccagcatcaaat 930
Qy 868 CCCAAGTTCTCATAACCTGATGAAGAGAG:GAGCACGAGAAACACTGGTCGGGCAATTCTCA 927
Db 931 cccaagttctcatacctcgtatgaagagg:jaagcacaagtatgtgcagggaattcttga 990
Qy 928 ATTCACATTTTATTCATTAATGTTGGGG:ATTTTTCAGCTCCGAGCTGGTGGAAGAAT 987
Db 991 attccattttattccataaacctgttggtg:atttttaagttacggtctcggagaggaat 1050
Qy 988 TAGCATTCAGGTGTCCCAACCTCTCCCTCG:FGATCCGGATCAAGATGCGACCTACTTTGG 1047
Db 1051 cagcatcaggtgtcccaacctcctctac:ggatccggtatcaggtatgaacatacttgg 1110
Qy 1048 GCCTTTCAAAGTTCAGGACATAGACTGAG:ACTCATTTTCGTGGAAACATAGCATGGATGTC 1107
Db 1111 ggcctttaagttcagatagattgag:cccagtttttggagtggt---atgtaatttc 1167
Qy 1108 CTAGATGTTGGAAACTCTTANAAA:-----ATGGATGATGCTATACATGTGTAGA 1160
Db 1168 ctggatgcttggaaacatttttaaaaa:igccaaagaagatgtatatagggtgtgaga 1227
Qy 1161 CTACTAAGAGACATGGCCACGGGTATG:AACTCACAGCCCTCTCTCTTGAAGCCTGTAC 1220
Db 1228 ctactaagaggcatggcccaacggtaca:gactcagtatccatgctcttgaccttgtag 1287
Qy 1221 AGTTGCTGTATATGTAAGCTCCATAGGTG:YGTGTAGATTCATGGTG-ATTACACAACGGT 1279
Db 1288 agaacacgcgtattttacagccagtgggag:tggtagactcatggtgtgttacacaatggt 1347
Qy 1280 TTTTACAAATTTGTATGATGTTTCCCTAAGAA:TTGAACACAGATGGGAGGATATTCGATGC 1339
Db 1348 ttttaaaatttgtatgaattcctt-agaattcaaacagatggaacattacggtttgac 1406
Qy 1340 TTATGAAAACCTTACACGTGAGCTATGGA:AGGGGCTCACAGTCTCTGGGCTCTTAACCCCTG 1399
Db 1407 ctatagagaacatgcattggcctatggg:-----ttggtccctg 1450
Qy 1400 GACATGTCCCACTGAGAACCTTGAAATTA:AGAAGATGCCATGTCTATTCGAAAGAATGAT 1459
Db 1451 gtcattgtccctctcgcagct-agaatgg:igagggtgtcatct-agcgcgaattgaagat 1508
Qy 1460 AGTGTGAAGGGTTAAGTCTTTTGAATGT:TTACATFTGGCTGGGACCTGCAAAATAGTTC 1519
Db 1509 catctgaagggggaaaattcttttgaattggttacatcatcgtcggaaacctgcataaaatac- 1567
Qy 1520 TTTTTCATATGAGGAGAGAAAAATATA:GTATTTTATATAATGCTCTAAAGTTATATT 1579
Db 1568 -tttttctaagaggagag-aaaataatgtatttttataataataatcatcaagtttatatt 1624

Qy 1580 TCAGGTGTAATGTTTCTGTGCAAAAGTTTGT:TAATATATATTTGTGCTATAGTATTGAT 1639
Db 1625 tcagatgtaatgtttcttcttgcaagatttga:aatatatatttgcctatagttattgat 1684
Qy 1640 TCAAAATATTTAAATAATGCTCTGTTGACAT:ATTTAAATGTTTAAATGTFACAGATGTA 1699
Db 1685 tcaaaaataattaaaaatgctctgctgttgac:atatttaagtgttttaaatgtcacagacata 1744
Qy 1700 TTTTAAGTGGTCACTTTGTAATTTCCCTGTG:-----AAGGTACTCGTAGCTAAGGGGGCAGA 1754
Db 1745 ttttaactgggtgcactttgtaaatccctggg:aaaccttcagctaaaggaggggaaaaaa 1804
Qy 1755 ATACTGTTTCTGTGTGACCCACATAGTGTAG:TTTATTTCTTTTAACTTAATAGAG-GT 1813
Db 1805 atgttgtttcctaataatcaaatgcagtata:ttcttccttcttttaagttaatagattt 1864
Qy 1814 CTTGAGACTTGTCAAAACTATGCAAGCAAAAT:AAATAAATAAATAAATAATGAATATCTTT 1873
Db 1865 tttcagacttgcgaagcctgtgc-----:aaaaaaattaaatggatgcctt 1910
Qy 1874 GAATAATAAGTAGGATGTGGTCACCAGGTGC:CTTTCAAAATTTAGAAAGCTAAATGACTTTT 1933
Db 1911 gaataataagcaggatgttggccaccagg:tgcccttccaatttagaaactaaattgacttt 1970
Qy 1934 AG-GAGCTGACATAGCAAAAGGATACATA:ATAGGCTACTGAAATCTGTCAGGAGTAT 1992
Db 1971 agaaactgacatgcccacaaaggatcacata:atgggcccactg-aaactgtccaagtag 2029
Qy 1993 TTATGCAATTAATTGAACAGGTGCTTTT:TTTACAGAGCTACAAATTTGTAATTTGTTT 2052
Db 2030 tlatataatgttgaacaggtg--ttttccaca:agtgccgcaaatgtgaccttt----- 2082
Qy 2053 CTTTCTTTTCCCATAGAAAATGTACTATAG:TTTATCAGCCAAAACAAATCCACTTTTAA 2112
Db 2083 -tttttttttccaataagaaagtattag:tggttttatcagcaaaaaagccaatttta 2141
Qy 2113 ATTTAGTGAAGTTATTTTATTATCTACTGT:ACAAATAAAGCATTTGTTCTGAATGGCATTT 2172
Db 2142 atttagtaaatgtta--tcttatactgtaca:ataaaaaaacattgcctttgaatttaatt 2198
Qy 2173 TTTGGTACTTAAAA 2186
Db 2199 ttttggatacaaaa 2212
RESULT 9
V70285
ID V70285 standard; DNA; 2274 BP.
XX V70285;
XX AC
XX DT
XX 11-FEB-1999 (first entry)
XX Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.linsert.
DE Human; osteoprotegerin binding protein; OPg binding protein; arthritis;
KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODA;
KW hypercalcaemia; osteoclast differentiation and activation receptor;
KW Paget's disease; ss.
XX OS
XX Homo sapiens.
XX FH
XX Key Location/Qualifiers
XX CDS 185..1138
XX FT
XX /*tag= a
XX FT
XX /product= "osteoprotegerin binding protein"
XX PN
XX WO9846751-Al.
XX PD
XX 22-OCT-1998.
XX PF
XX 15-APR-1998; 98WO-US07584.

XX 30-MAR-1998; 98US-0052521.
PR 16-APR-1997; 97US-0842842.
PR 23-JUN-1997; 97US-0880855.
XX (AMGE-) AMGEN INC.
XX Boyle WJ;
XX WPI; 1998-594578/50.
DR P-PSDB; W83195.
XX Nucleic acid encoding osteoprotegerin binding protein - useful for,
PT e.g. treating bone diseases by modulating osteoclast differentiation
PT and for diagnosis
XX Claim 1; Fig 4; 47pp; English.
XX The present sequence encodes human osteoprotegerin (OPG) binding protein.
CC Host cells transfected with vectors containing nucleic acid molecules
CC encoding OPG binding protein are used to produce recombinant OPG binding
CC protein. OPG binding protein is used in binding assays to determine
CC osteoprotegerin (OG) in biological samples; to screen for specific
CC binding agents (particularly agonists and antagonists, including
CC intracellular proteins); to raise Ab (useful in immunoassays for
CC detection of OPG binding protein) and to identify compounds that
CC modulate binding of OPG binding protein to osteoclast differentiation
CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG
CC binding protein can be used to detect OPG binding protein-encoding
CC sequences, e.g. screening for related sequences, also to produce
CC transgenic animal models, while complementary sequences are used for
CC antisense regulation of OPG binding protein expression. Modulators of
CC OPG binding protein, particularly soluble forms of OPG binding protein
CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
CC disease, periodontal disease, osteoporosis, loosening of prostheses,
CC optionally in combination with agents that promote bone growth.
XX Sequence 2274 BP; 658 A; 463 C; 523 G; 630 T; 0 other;

Query Match 51.18; Score 1118.8; DB 19; Length 2274;
Best Local Similarity 76.38; Pred. No. 3.7e-253;
Matches 1659; Conservative 0; Mismatches 437; Indels 78; Gaps 20;

XX	36	GCCTGGCGGGAGTCTGCTCGCGGTGGGTGCCGAGGAAGGAGAGACGATCGGGAG	95
Db	94	ggctccgcgcagcctccgagttggccgcagacagaagaggagggagggagaggga	153
Qy	96	CAGGCGCGCGAATCCCGGGCGCC--GGGCCATGGCGCGGCGCAGCGAGACTACGGCAA	153
Db	154	ggagagctccgaagcgaagggccgagcgccatgcgcgcgcagcagagactacacaa	213
Qy	154	GTACTTGGCAGCTCGGAGGAGATGGGACGGCGCGCGCGTCCACAGAGGGTCCGCT	213
Db	214	gtacctgctgctcgaggagatggcgcgcccgagcccgagcccgacagggccccc	273
Qy	214	GCACCCCGCGCTCTGTCACCGGCTCCGGCGCGCGCACCGCGCGCTCCCGTCCATGTT	273
Db	274	gcacgccccgc---cgccgcttgccgcgcaccagccccccgcgcctccgcctcatgtt	330
Qy	274	CCTGCGCCTCTGGGGCTGGGACTGGGCGAGGTGGTCTGTCAGCATCGCTCTGTTCTGTA	333
Db	331	cgtgccccctcgggctgggctgggagagtgctgtctgcagcgtcgccctgtctctota	390
Qy	334	CTTTCAGGCGGAGATGGATCTTAACAGATATCAGAAGACAGACTCATCTGTTTATAG	393
Db	391	tttcagagcgcagatggatcctaatagaatatcagaagatggcaactcactgcatttatag	450
Qy	394	AATCTTGAGATCCATGAAACCGAGTTTGCAGGACTCGACTCTGGAGACTGAACACAC	453
Db	451	aatttggactcctgaataatgcagattttcgaagacacaaactctggagagtcagatac	510

Qy	454	-----ACTACCTGACTCTCTGCAGGAGGATGAACAAGCCCTTTCAGGGGCGCGTGAGAA	507
Db	511	aaatataacacctgattcatgtaggaataaaacagcccttcaadgagctgcaaaa	570
Qy	508	GAACTGCAACACATTTGTGGGGCACAGCGCTTCTCAGGAGCTCCAGCTATGATGGAGG	567
Db	571	ggaattacaacatatcgttgatcacagacatcagagcagagaaagcagctggtgatgg	630
Qy	568	CTCATGTTGGATGTGGCCCGCAGCGCAAGCCCTGAGGCCCGCCAGCCATTTTGACACCTTAC	627
Db	631	ctcatggttagatctggcgaagagagcaagcttgagagctcagcctttgtcctatctac	690
Qy	628	CATCAATGCTGCCAGCATCCATCGGGTTCCTCAATAAGTCACTCTGCTCTTCTGGTACCA	687
Db	691	tattaatgccacgacatccccatctggttcccaataaagtgatgctctctcttggtagca	750
Qy	688	CGATCGAGGCTGGCCCAAGATCTTAACATGACGTTAAGCAACGAAACCTAAAGGTTAA	747
Db	751	tgatcggggttgcccaagatctccaacatgacttttagcaatggaaaactaatagttaa	810
Qy	748	CCAAGATGGCTTCTATTACCTGTACGCCCAACATTTGCTTCGGCATCATGAACATCGG	807
Db	811	tcaggatggctttattacactgtatgcacacatttgcttctgcacatcatgaaactcagg	870
Qy	808	AAGCTTACCTACAGACTATCTTCAGCTGATGGTGTATGTCTGTTAAACCAACATCAAAAT	867
Db	871	agacctagctacagatattctcaactaatgggtcactcaataaaccagcatcaaaa	930
Qy	868	CCCAAGTTCCTCATAACTGATGAAAGGAGGAGGAGCACCAGAAACCTGGTCGGCAATTCTGA	927
Db	931	cccaagctctcataccctgatgaaagagagaaagcaccagatattggtcagggaaattctga	990
Qy	928	ATTTCCACTTTTATTCATAAATTTGGGGATTTTTCAGCTCCGAGTGTGTGAAGAAT	987
Db	991	attccatttttccataaacagtgggagatttttaagttagctgctggagagaaat	1050
Qy	988	TAGATTCAGGTGTCCAAACCTTCCCTGCTGGATGCCGGATCAAGATGGGAGCTACTTTGG	1047
Db	1051	cagcatcgaggtctccaaacctcttactggtacccgagatccgagatgcaacatacttgg	1110
Qy	1048	GGCTTTCAAAGTTCAGGACATAGACTCAGACTCATTTTCGTGGAACATTAGCATGGATGTC	1107
Db	1111	ggctttaaagtcgcagatatagattgagccccagtttttggagtggt---atglatcttc	1167
Qy	1108	CTAGATGTTTTGGAACCTCTTAAAAA-----ATGGATGATGCTATACATGTGTAAAGA	1160
Db	1168	ctgagatgttggaaacattttttaaacaagcccaagaaagatgtatatagtggtgaga	1227
Qy	1161	CTACTAGAGACATGGCCCGCGGTGTATGAACCTCACAGCCCTCTCTCTTGAGCCTGTAC	1220
Db	1228	ctactaagagggcatggccccaaacggtacacgactcaglatccatgctcttgacctgtag	1287
Qy	1221	AGTTTGTGTATATGTAAGTCCATAGGTGATGTAGATTCATGTTG-ATTACACACCGT	1279
Db	1288	agaacacgcglatttacagccagtgggagatggttagctcatggtggttctacaaatggt	1347
Qy	1280	TTTACAAATTTTGAATGATTTCTTAAAGATTTGAACCTGAAACCTGGGAGAGGATTCGATGC	1339
Db	1348	ttttaaattttgtaataaattcct-agaattaaacagattggagcaattacgggttgac	1406
Qy	1340	TTATGAAAACTTACAGCTGAGCTATGGAAGGGGGTCCACGCTCTCTGGGTCTAACCCCTG	1399
Db	1407	ctlatgagaacgcatgtgggctatggggggg-----ttggctccctg	1450
Qy	1400	GACATGTCGCACTCAGAACCTTGAATTAAGAAGATGCCATGTCATTTGCAAGAATGAT	1459
Db	1451	gtcatgtgcccccttcgcagct-gaagtggagaggggtgctcatct-agecgaattgaagat	1508
Qy	1460	AGTGTGAAGGGTAAAGTCTTTTCAATTTGTTACATTTGGCTGGGAGCCCTGCAAAATAAGTTC	1519
Db	1509	catctggaaggggcaaatctcttttgaaattgttcatcatcagctggaaacctgcaaaaaaac-	1567
Qy	1520	TTTTTTTCTAATGAGGAGAGAAAAATATATGTTATTTTATATATGTTCTAAAGTTATAT	1579

CC activity, and screening for receptors to OBM which mediate its function.
CC These substances can then be used in the treatment of disorders of bone
CC function and calcium metabolism. The antibodies can be used for assay
CC of the protein, for investigative and diagnostic purposes, and as
CC components of drugs.
XX
XX

SQ Sequence 951 BP; 231 A; 267 C; 248 G; 205 T; 0 other;

Query Match 43.4%; Score 951; DB 19; Length 951;
Best Local Similarity 100.0%; Pred. No. 6e-214;
Matches 951; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 ATGCGCGGCGGCGGAGACTACGGGAAATACCTGCGGAGCTCGGAGAGATGGGCGAGC 184
Db 1 atgcgcggcgccagccgagactacggcaat; tacctgcgagctcgaggagatggcgagc 60
Qy 185 GCGCGCGGCTCCACACAGAGGTCGCTGCACCCGCGCTTCGACCCGCTCGGCGG 244
Db 61 ggcgcggcgctccacacaggggtccgct; jcacccgcgcgctcttgacccggtcccgcg 120
Qy 245 CCGCACCGCGCGCTCCGCTCCATGTTCTGCGCCCTCCTGGGCTGGGAGCTGGCGCAG 304
Db 121 cgcacccgcgcctccgctccatgttctgcccctctgggctgggactgggcccag 180
Qy 305 GTGGTCTCAGATCGCTCTGTTCCTGTAATTTAGATCTTGAGCGCGAGATGCTTAACAGAAAT 364
Db 181 gtggtcgcagcatcgtctgtctctgtacttctgagcgcagatggtacttaacagaata 240
Qy 365 TCAGAGACAGACTCAGCTCTGTTTATAGATCTTGAGCTCCATCCATCAAAACGCGTTTG 424
Db 241 tcagaagacagactcaactgttttatagatccttgagactccatgaaacagagtttg 300
Qy 425 CAGACTCGACTCTGGAGAGTGAACACACTTACCTGACTCTCTGAGGAGGATGAACAA 484
Db 301 caggactcactctggagagtgaagacacactacctgactcctgcaggaggtgaacaa 360
Qy 485 GCCTTTACGGGCGCGCTGCAGAGGAATCAACACATTTGTTGGGCCACAGCGCTTCTCA 544
Db 361 gcccttcaggggcgctgcagaggaactgcaacacattgtgggcccacagcgtcttca 420
Qy 545 GGAGCTCAGCTATGATCGAAGGCTCATGTTGGATGTGGCCCGCGAGCGCAAGCTGAG 604
Db 421 ggagctcagctatgatggaaggctcatggttgatgtggccagcgaggcaagcctgag 480
Qy 605 GCCAGGCAATTTGCACACTCAGCATCAATGCTGCAGCATCCCATCGGTTCCCATAAA 664
Db 481 gccagccatttgcacacctcaccatcaatgctgccagcatcccatcggttcccataaa 540
Qy 665 GTCACTCTGCTCTTGTGTACGATCGAGGCTGGGCGCAAGATCTTAACATGACGTTA 724
Db 541 gtaactctgctcttggtaccagatcagagctggcccaagatcttaacatgacgtta 600
Qy 725 AGCAACGAAACTAAGGGTTAAACCAAGATGGCTTCTATTACCTGTACGCCCAACATTTGC 784
Db 601 agcaacgaaactaaaggttlaaccaagatggcttctattaccctgtacgccaaacttgc 660
Qy 785 TTTGGCATCATGAACATCGGGAAGCGTACCTACAGACTATCTACGCTGATGTGTAT 844
Db 661 ttctggcaatcatgaacatcgggagcgtaactacagactatcttcagctgatgtgat 720
Qy 845 GTCGTTAAACGAGCATCAAAATCCCAAGTTCTCATACCTGATGAAAGGAGGAGCAGC 904
Db 721 gtcgttaaacacagcatcaaaatcccaagtctctataacctgaataagggagggagcag 780
Qy 905 AAAAAGTGGTGGGCAATTCGAATTCCTTAATTCCTTAATTCCTTAATTCCTTAATTCCT 964
Db 781 aaaaactggtcggaattctgaattcccttttattccataaaatgttgggggatttttc 840
Qy 965 AAGCTCCGAGCTGTGAGAAATATAGCATTCAGTGTGTCACACCTTCCTCTGCTGATCCG 1024
Db 841 aagctccgagctgttgaagaataatagcattcaggtgttccaaaccttccctgctgataccg 900

Qy 1025 GATCAAGATCGGAGCTACTTTTGGGCTTTCAAAAGTTTCAGGACATAGACTGA 1075
Db 901 gatcaagatcgagctactttggggtttcaaaagtttcaggacatagactga 951

RESULT 12

ID Z99965 standard; DNA; 951 BP.

XX Z99965;

DT 25-JUL-2000 (first entry)

XX DNA encoding a murine osteoprotegerin ligand (OPGL).

XX Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
KW tumour necrosis factor receptor; type II transmembrane protein;
KW osteoclast differentiation; CSF-1; osteoclast activator;
KW immune response; osteoporosis; bone resorption; ss.

OS Mus musculus.

XX Key Location/Qualifiers
FH CDS 1..951

FT /*tag= a
/product= "osteoprotegerin ligand"

XX WO200015807-A1.

XX PD 23-MAR-2000.

XX PF 13-SEP-1999; 99WO-DK00481.

XX PR 15-SEP-1998; 98DK-0001164.

XX PR 02-OCT-1998; 98US-0102896.

XX (MEBI-) M & E BIOTECH AS.

XX Halkier T, Heaning J;

DR WPI: 2000-271444/23.

XX P-PSDB; Y84418.

PT In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used

XX to treat, prevent and ameliorate osteoporosis -

PS Disclosure: Page 79-81; 110pp; English.

XX The present sequence encodes a murine osteoprotegerin ligand (OPGL).
CC Osteoprotegerin is a secreted member of the tumour necrosis factor
CC receptor family, which blocks osteoclastogenesis in a dose dependent
CC manner. The OPGL protein is synthesised as a type II transmembrane
CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
CC is a potent osteoclast differentiation factor when combined with CSF-1.
CC It is not capable of inducing osteoclast differentiation in the absence
CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
CC specification describes a method for the in vivo down-regulation of
CC OPGL activity in an animal. The method comprises using at least one OPGL
CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
CC an immune response in the animal. The method and OPGL polypeptide are
CC useful for treating, preventing and ameliorating osteoporosis or other
CC diseases or conditions characterised by excessive bone resorption.

XX Sequence 951 BP; 231 A; 267 C; 248 G; 205 T; 0 other;

Query Match 43.4%; Score 951; DB 21; Length 951;
Best Local Similarity 100.0%; Pred. No. 6e-214;
Matches 951; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 ATGCGCGGCGGCGGAGACTACGGGAAATACCTGCGGAGCTCGGAGAGATGGGCGAGC 184
Db 1 atgcgcggcgccagccgagactacggcaat; tacctgcgagctcgaggagatggcgagc 60

QY 185 GGCCCGCGCTCCACACAGAGGCTCCGCTGCACCCGCGCTTCTGCACCGGCTCCGCGC 244
DB 61 gggcccgccgctccacacagggctccgctgcaccccgccctctctgcacggctcccgcg 120
QY 245 CCGCCACCGCGCCCTCCGCTCCATGTTCTCTGCGCCCTCTGGGGCTGGGACTGGGCGAG 304
DB 121 ccgcccacgcgcctcccgctccatgttcttgccctctgggctgggactgggcccag 180
QY 305 GTGGTCTGACGATCGCTCTGTTCCTGTACTTTCGAGCGCAGATGATCTTAACAGAAATA 364
DB 181 gtggtcgcagatcgctctgttctctgtactttcgcagcgcagatggatcctaacaagaata 240
QY 365 TCAGAGACAGCACTCACTGCTTTTATAGAAATCCTGAGACTCCATGAAGCGCAGGTTTG 424
DB 241 tcagaagacagcactcactgctctttatagaatcctgagactccatgaaaacgcagggttg 300
QY 425 CAGGACTCGACTCTGGAGAGTGAAGACACACTACTGACTTCCTGCAGAGGATGAACAAA 484
DB 301 caggactcgacttgagagtgagacacacactacctgactcctgcagagagatgaaacaa 360
QY 485 GCGTTTCAGGGCGCGTGCAGAGGAAGTCAACACATTTGGGGCCACAGCGCTTCTCA 544
DB 361 gcttttcagggggccgtgcagaaggaactgcaacacattgtggggccacagcgttctca 420
QY 545 GGAGCTCCAGCTATGATGGAGGCTCATGTTGGATGTGGCCGAGCGAGCAAGCCTGAG 604
DB 421 ggaagctccagctatgatggaagctcatggttgatgtggccagcgaggaagcctgag 480
QY 605 GCCAGCCATTTGCACACCTTCACCATCAATGCTGCCAGCATCCATCGGGTTCCTCAATAA 664
DB 481 gccagccatttgcacaccltccacatcaatgctgcagcagctccatcgggttcccataa 540
QY 665 GTCACCTCTGCTCTTCTGTACCAACGATCGAGGCTGGGCCAAGATCTCTAACATGACGTTA 724
DB 541 gtcactctgtcctcttggtaccacgactcagagctgagcgtggccaagatccttaacatgacgtta 600
QY 725 AGCAACGGAAACTAGGGTTACCAAGATGGCTTCTATTACCTGTACGCCACACATTTGC 784
DB 601 agcaacggaaaactaagggttaccacgaagtggcttctattacactgtacgcacacatttcg 660
QY 785 TTTTCGGCATCATCAACATCGGAAGCGTACCTACAGACTATCTTCAGCTGATGGTGTAT 844
DB 661 ttcgcgacatcatgaacacatcggaagcgtacctcacagactatcttcagctgagtgtgat 720
QY 845 GTCGTTAAACACAGCATCAAAATCCCAAGTTCTCATAACTGATGAAGAGGAGGAGCAGC 904
DB 721 gtcgttaaaacacagatcaaaaatcccgaagttctcataaacctgatgaaagagggagcacg 780
QY 905 AAAAATGTCGGGCAATTTCTGAATTTCCACTTTTATTCATAAATGTTGGGGATTTTC 964
DB 781 aaaaactggtcggggcaattctgaaattccacttttattccataaatggtggggatttttc 840
QY 965 AAGCTCCGAGCTGGTGAAGAAATAGCATTCAGGTGTCGAACCTTCCCTGCTGGATCCG 1024
DB 841 aagctccgagctggtgaagaaattagcattcagggtgtccaaaccttccctgctggatccg 900
QY 1025 GATCAAGATTCGAGCTACTTTTGGGGCTTTTCAAAAGTTTCAGGACATAGACTGA 1075
DB 901 galcaagatgcagcgtacttttggggcttttcaaaagtttcaggagacatagactga 951

RESULT 13
ID 249024
XX 249024 standard; DNA; 951 BP.
AC 249024;
XX 31-MAR-2000 (first entry)
DT Osteoclast formation promoting factor coding sequence.
XX OBM-BP; OBM binding protein; osteoclast formation promoting factor;
KW

bone metabolic disease; osteoporosis; therapy; ss.
Mus sp.
JPl1332581-A.
07-DEC-1999.
20-OCT-1998; 98JP-0316973.
24-MAR-1998; 98JP-0076232.
(SNOW) SNOW BRAND MILK PROD CO LTD.
(SANY) SANKYO CO LTD.
WPI; 2000-091362/08.
A new protein, a DNA and its application -
Example 1; Page 13; 18pp; Japanese.
This sequence encodes the osteoclast formation promoting factor (OBM).
The invention relates to an OBM binding protein (OBM-BP). The protein is
useful as a preventive and/or treating agent for bone metabolic diseases
such as osteoporosis. Substances which inhibit the binding of OBM to
OBM-BP can be used as biochemical reagents.
Sequence 951 BP; 231 A; 267 C; 248 G; 205 T; 0 other;

Query Match 43.4%; Score 951; DB 21; Length 951;
Best Local Similarity 100.0%; Pred. No. 6e-214;
Matches 951; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 125 ATGCGCGGGCGCAGCGGAGACTACGGCAAGTACCTGCGCAGCTCGAGGAGATGGGCGC 184
DB 1 atgcgcggggccagccgagactacgcgcaagtacctgcgcagctcgagagatgggcgcg 60
QY 185 GGCCCGCGCTCCACACAGAGGCTCCGCTGCACCCGCGGCTTCTGCACCGGCTCCGGCG 244
DB 61 gggcccgccgtccacacagagggtccgctgcaccccgccctctgcacggctccggcg 120
QY 245 CCGCACCGCGCGCTCCCGCTCCATGTTCTGTGGCCCTTCCTGGGGCTGGGACTGGGCCAG 304
DB 121 ccgcacacgcgcctcccgctccatgttctgacctggtgacctggtgggactgggcag 180
QY 305 GTGCTCTGCACATCGCTCTGTCTCTGTACTTTCAGCGCAGCATGATCCTTAACAGAAATA 364
DB 181 gtgctctgcagcatcgctctgttctctgtactttcgcagcgcagatggatcctaacagaata 240
QY 365 TCAGAAGACAGCACTCACTGCTTTTATAGAAATCCTTGAGACTCCATGAAGCGCAGGTTTG 424
DB 241 tcagaagacagcactcactgctctttatagaatcctgagactccatgaaacgcagggttg 300
QY 425 CAGGACTCGACTCTGGAGAGTGAAGACACACTACTGACTTCCTGCAGGAGGATGAACAAA 484
DB 301 caggactcgacttgagagtgagacacacactacctgactcctgcagggagtgaaacaa 360
QY 485 GCCTTTTCAGGGCGCGTGCAGAGGAAGTGAACACATTTGTGGGCCACAGCGCTTCTCA 544
DB 361 gcttttcagggggccgtgcagaaggaactgcaacacattgtgcagcatccctcggttcccataa 420
QY 545 GGAGCTCCAGCTATGATGGAGGCTCATGTTGGATGTGGCCGAGCGAGCAAGCCTGAG 604
DB 421 ggaagctccagctatgatggaagctcatggttgatgtggccagcgaggaagcctgag 480
QY 605 GCCAGCCATTTGCACACCTTCACCATCAATGCTGCCAGCATCCATCGGGTTCCTCAATAA 664
DB 481 gccagccatttgcacaccltccacatcaatgctgcagcagctccatcgggttcccataa 540
QY 665 GTCACCTCTGCTCTTCTGTACCAACGATCGAGGCTGGGCCAAGATCTCTAACATGACGTTA 724
DB 541 gtcactctgtcctcttggtaccacgactcagagctgagcgtggccaagatccttaacatgacgtta 600
QY 725 AGCAACGGAAACTAGGGTTACCAAGATGGCTTCTATTACCTGTACGCCACACATTTTC 784
DB 601 agcaacggaaaactaagggttaccacgaagtggcttctattacactgtacgcacacatttcg 660
QY 785 TTTTCGGCATCATCAACATCGGAAGCGTACCTACAGACTATCTTCAGCTGATGGTGTAT 844
DB 661 ttcgcgacatcatgaacacatcggaagcgtacctcacagactatcttcagctgagtgtgat 720
QY 845 GTCGTTAAACACAGCATCAAAATCCCAAGTTCTCATAACTGATGAAGAGGAGGAGCAGC 904
DB 721 gtcgttaaaacacagatcaaaaatcccgaagttctcataaacctgatgaaagagggagcacg 780
QY 905 AAAAATGTCGGGCAATTTCTGAATTTCCACTTTTATTCATAAATGTTGGGGATTTTC 964
DB 781 aaaaactggtcggggcaattctgaaattccacttttattccataaatggtggggatttttc 840
QY 965 AAGCTCCGAGCTGGTGAAGAAATAGCATTCAGGTGTCGAACCTTCCCTGCTGGATCCG 1024
DB 841 aagctccgagctggtgaagaaattagcattcagggtgtccaaaccttccctgctggatccg 900
QY 1025 GATCAAGATTCGAGCTACTTTTGGGGCTTTTCAAAAGTTTCAGGACATAGACTGA 1075
DB 901 galcaagatgcagcgtacttttggggcttttcaaaagtttcaggagacatagactga 951

QY 725 AGCAACGGAAACTAAGGTTAACCAAGTGGCTTCTATTACCTGTACGCCAACATTTGC 784
 Db 601 agcaacggaactaagggttaaccaagctggcttctattactgtacgccaacatttgc 660
 QY 785 TTTTCGCATCATGAACATPCGGGAAGCGTACCTACAGACTATCTCAGCTGATGGTAT 844
 Db 661 ttctggcatcatgaacacacggaagcgtacctacagactatctcagctgagtgtat 720
 QY 845 GTCTGTTAAACAGCATCAAAATCCCAKTTCTATAACCTGATGAAGGAGGAGCAGC 904
 Db 721 gtcgttaaacacagatcaaaatcccaatctctataacctgatgaagaggagagcag 780
 QY 905 AAAAAGCTGTCGGGCAATTCGAATTCCTTTTATTCATATAATGTTGGGGGATTTTC 964
 Db 781 aaaaactgctggcggaattctgaattccrctttattccataaatgttggggattttc 840
 QY 965 AAGCTCCGAGCTGGTGAAGAAATTAGCACTCAGGTGTCCAACTTCCCTGCTGGATCCG 1024
 Db 841 aagctccgagctggtgaagaaattagcatcagggtgccaaaccttccctgctggatccg 900
 QY 1025 GATCAAGATGCCAGCTACTTTGGGGCTTCAAAGTTTCAGGACATAGACTGA 1075
 Db 901 gatcaagatgcagctactcttggggcttcaaaagttcaggacatagactga 951

RESULT 14
 V69898
 ID V69898 standard; cDNA to mRNA; 731 bp.
 XX V69898;
 AC
 XX
 DT 10-FEB-1999 (first entry)
 XX
 DE Nucleic acid encoding a murine OCIF-binding molecule (OBM).
 XX
 KW Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
 KW osteoclast; bone absorption facto.; bone disorder; calcium metabolism;
 KW mouse; ss.
 OS
 XX Mus sp.
 XX
 FH Key Location/Qualife:s
 FT CDS 1..735
 FT /*tag= a
 XX
 PN WO9846644-A1.
 XX
 PD 22-OCT-1998.
 XX
 PF 15-APR-1998; 98WO-JP01728.
 XX
 PR 02-DEC-1997; 97JP-0332241.
 PR 15-APR-1997; 97JP-0097808.
 PR 09-JUN-1997; 97JP-0151434.
 PR 12-AUG-1997; 97JP-0217897.
 PR 21-AUG-1997; 97JP-0224803.
 XX
 PA (SNOW) SNOW BRAND MILK PROD CO L/D.
 XX
 PI Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
 PI Nakagawa N, Takahashi C, Tomoyasu A, Tsuda E;
 PI Washida N, Yamaguchi K, Yano K, Yasuda H;
 XX
 DR WPI: 1998-594563/50.
 DR P-PSDB: W83019.
 XX
 XX Protein binding to osteoclastogenesis inhibitory factor - useful
 PT for, e.g. treatment and investigation of disorders of bone and
 PT calcium metabolism
 XX
 PS Example 28; Page 121; 151pp; Japanese.
 XX

CC The present sequence encodes an osteoclastogenesis inhibitory factor
 (OCIF)-binding molecule (OBM). The protein promotes and supports the
 CC separation and maturation of osteoclasts in the presence of bone
 CC absorption factors such as calcitriol or parathyroid hormone (PTH).
 CC OBM is isolated from stroma cells cultured in the presence of a bone
 CC absorption factor by separation and solubilisation of membrane proteins
 CC then affinity chromatography using OCIF. It exists in a full-sequence
 CC form and a solubilised form (SOBM) which is a shorter chain. OBM may be
 CC used for screening potential inhibitors and modifiers of its biological
 CC activity, and screening for receptors to OBM which mediate its function.
 CC These substances can then be used in the treatment of disorders of bone
 CC function and calcium metabolism. The antibodies can be used for assay
 CC of the protein, for investigative and diagnostic purposes, and as
 CC components of drugs.
 XX
 SQ Sequence 735 BP; 205 A; 182 C; 179 G; 169 T; 0 other;

Query Match 33.5%; Score 735; DB 19; Length 735;
 Best Local Similarity 100.0%; Pred. No. 2.7e-163;
 Matches 735; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 341 GCCCAGATGCCTTACAGATATCAGAAAGACGAGCTCCTGCTTTTATAGAACTCTG 400
 Db 1 ggcagatggatcctaacagaaatcagaagacagcactcactgctttatagaactcg 60
 QY 401 AGACTCCATGAAACGCAGGTTTGCAGGACTCGACTCTGGAGAGTGAAGACACACTACT 460
 Db 61 agactccatgaaacgcaggtttgcaggactcgtgagagtgagagtcacactacct 120
 QY 461 GACTCTCGCAGGAGATGAACAAAGCCTTTTCAGGGGCCCTGCAAGAGAACTGCAACAC 520
 Db 121 gactcctcagagagatgaacaaagcctttcaggggcccgcgcagaaggaactgcaaac 180
 QY 521 ATTGTGGGCCACAGCGCTTCTCAGGAGTCCAGCTATGATGAAGGCTCATGCTTGGAT 580
 Db 181 attgtgggcccacagcgtcttcaggagctccagctatgatgaaaggctcaggtgat 240
 QY 581 GTGGCCCGCAGGAGCGCTGAGGCCAGCCATTTGCACACCTCACCTCAATGCTGCC 640
 Db 241 gtggcccagcagcagcgtgagcccagcatttgcacacctcaccatcaatgctgcc 300
 QY 641 AGCATCCCATCGGTTCCCATAAAGTCACTCTGCTCTTGTGGTACCACGATCGAGGCTGG 700
 Db 301 agcatcccatcggttcccataaagtcactctgctccttgggtaccacgacgcaggtgg 360
 QY 701 GCCAAGATCTTAACATGAGCTTTAAGCACGGAATAACTAAGGTTAACCAAGATGCGCTC 760
 Db 361 gccagatctctaactgacgttaagcaacggaaaactaagggttaaccaagatggcttc 420
 QY 761 TATTACCTGTACGCCAACATTTGCTTTCCGCATCATGAACATCGGGAGCGTACCTTACA 820
 Db 421 tattacctgtacgccaactttgcttctcggcatcatgaacatcgggaagcgtacactaca 480
 QY 821 GACTATCTTCAGCTGATGTTGTTATGCTTTAAACACGAGCATCAAAATCCCAAGTTCAT 880
 Db 481 gactatcttcagctgagt 540
 QY 881 AACCTGATGAAGGAGGAGGAGCAGCAAAAACCTGGTCGGGCAATTTCTGATTTCCACTTTAT 940
 Db 541 aacctgtgaaagaggaggagcagcaaaaaactggtcgggcaattctgaattccacttttat 600
 QY 941 TCCATAAATGTTGGGGGATTTTCAAGCTCCGAGCTGGTGAAGAAATATGACATTCAGGTG 1000
 Db 601 tccataaatgttgggggatttttcaagctccgagctggtgtgtgtgtgtgtgtgtgtgt 660
 QY 1001 TCCAACTTCCCTGCTGCTGATCCGATCAAGATGCCAGCTACTTTGGGGCTTTCAGAGTT 1060
 Db 661 tccaaaccttccctgctggtatccggtatccagatgcgacgtacttcttgggggtttc 720
 QY 1061 CAGGACATAGACTGA 1075
 Db 721 caggacatagactga 735

RESULT 15

V41378
ID V41378 standard; cDNA; 954 BP.
XX
AC V41378;
XX
DT 08-OCT-1998 (first entry)
XX
XX NF- κ B receptor activator RANK ligand (RANKL) encoding cDNA.
DE
XX RANK; necrosis factor- κ B; NF- κ B; receptor activator; human;
KW immune response; inflammatory response; toxic shock; sepsis;
KW RANKL; RANK ligand; tumour necrosis factor; TNF; ss.
XX
OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 1..954

FT /*tag= a

FT /product= "human RANKL (ligand for RANK)"

PN W09B28426-A2.

XX

PD 02-JUL-1998.

XX

PF 22-DEC-1997; 97WO-US23775.

XX

PR 14-OCT-1997; 97US-0064671.

PR 23-DEC-1996; 96US-0059978.

PR 07-MAR-1997; 97US-0813509.

XX

PA (IMNV) IMMUNEX CORP.

XX

PI Anderson DM, Galibert LJ, Maraskovsky E;

XX

WPI: 1998-377657/32.

DR P-PSDB; W69957.

XX

PT New isolated ligand for receptor activator of NF- κ B B - used to
PT develop products for augmenting an immune response for inhibiting an
PT inflammatory response and for protection of cells

XX

PS Claim 25; Pages 59-60; 80pp; English.

XX

CC This cDNA encodes a human RANKL, a ligand for the RANK (receptor
CC activator of necrosis factor- κ B) (NF- κ B) polypeptide. RANK is a
CC member of the tumour necrosis factor (TNF) family. A soluble RANK
CC may be used for inhibiting activation of NF- κ B, by contacting a cell
CC expressing membrane-associated RANK with a soluble RANK which binds to
CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
CC used to induce maturation of dendritic cells and enhance their
CC allo-stimulatory capacity, thereby augmenting an immune response. The
CC soluble RANK polypeptide composition may also be used for regulating an
CC immune or inflammatory response. Inhibition of NF- κ B by RANK antagonists
CC may be useful in ameliorating negative effects of an inflammatory
CC response that result from triggering of RANK, e.g. in treating toxic
CC shock or sepsis, graft-versus-host reactions, or acute inflammatory
CC reactions. They can also be used in adjunct therapy for disease
CC characterised by neoplastic cells that express RANK. RANKL polypeptides
CC can also be used to identify inhibitors of RANK and thus inhibitors of
CC an inflammatory response, and also for protecting RANK-expressing cells
CC from the negative effects of chemotherapy or the presence of high levels
CC of TNF- α . The products can also be used for detection and drug
CC screening.

XX

SQ Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;

Query Match 30.4%; Score 666.2; DB 19; Length 954;
Best Local Similarity 82.5%; Pred No. 4.2e-147;
Matches 790; Conservative 0; Mismatches 158; Indels 9; Gaps 2;

QY 125 ATGGCCGGCCGACGCGAGAGTACGGCAAGTACCTGCCAGCTCGGAGGAGATGGGACG 184
DB 1 atgcccgcgcagcagagactacaccaagtacctggtgctcgaggagatggcgccg 60
QY 185 GGGCCCGCGCTCCACACAGAGGTCGCGTGCACCCCGCGCTTCTGCAACCGCTCCGGCG 244
DB 61 gcccgc 117
QY 245 CCGCCACCCCGCGCTCCCGCTCCATGTTCTGCGCCCTCTGGGGCTGGGACTGGGCGAG 304
DB 118 cagcccccgc 177
QY 305 GTGGTCTGCAGCATCGCTCTGTTCTCTACTTTCGAGCGCAGATGGATCTTAACAGATA 364
DB 178 gttgtctgcagcgtcgccctgttcttatttcagagcgcagatggatccctaagaata 237
QY 365 TCAGAGACAGCAGCTACTGCTTTTATAGAATCTGAGACTCCAGTAAACGCGAGTTTG 424
DB 238 tcagaagatggcactcactgcatttatagaatttgagactccatgaaaaatgcagatttt 297
QY 425 CAGGACTCGACTCTGGAGAGTGAACACACACACACACACACACACACACACACACAC 478
DB 298 caagacacacactctggagagtcagatacaaaaattaatcacctgattcattgagagaatt 357
QY 479 AACAAGCCTTTTCAGGGGCGGTGCAGAAAGAACTGCAACACATTTGTGGGCCAGGCGC 538
DB 358 aacagcgccttcaaggagctgtcaaaaggaattacaacatatctgttgatccacagcac 417
QY 539 TTCTCAGGAGCTCCAGCTATGATGGAAGGCTCATGGTTGGATGTGGCCAGGAGGCAAG 598
DB 418 atcagagcagagaaacgagtcggtggttcagtggttagatctgtgccaagagagcaag 477
QY 599 CCTGAGCCCGCAGCTTTCACACCTCACCATCAATGTGCTGCAGCATCCCATCGGTTCC 658
DB 478 ctggaagctcagccctttgtctcactcacttaataatgcacagacatcccatctggttcc 537
QY 659 CATAAAGTCACTCTGCTCTTGTGTACACGATCGAGGCTGGGCGCAAGATCTCTAACATG 718
DB 538 cataaagtgcgtctctctgttaccatgctggtggtggtggtggtggtggtggtggtggtggt 597
QY 719 ACGTTAGACACGAAACAACTAAGGTTAAACCAAGATGGCTTCTATTACCTGTACGCCAAC 778
DB 598 acttttagcaatggaaaactaatagtaataatcagagtggtcttttattacctgtatgccaac 657
QY 779 ATTTGCTTTTCGGCATCATGAACATCGGCAAGCTACAGACTATCTTCAGCTGATG 838
DB 658 atttgctttcgacatcatgaaacttcaggagacctagctacagagatatcttcaactaag 717
QY 839 GTGTATGCTGTTAAACACGAGCATCAAAATCCCAAGTCTCTCAATACCTGATGAAGAGGG 898
DB 718 gtgtactcactaaaccagcatcaaaatcccaagttctcaccctgatgaaagagga 777
QY 899 AGCACGAAAACTGGTGGGCAATCTCTGAATCCACTTTTATTCATTAATTTGGGGA 958
DB 778 agaccaagtattggtcaggggaattctgaattccattttttattccataaaacgttggtaga 837
QY 959 TTTTTCAGCTCCAGCTGCTGTCAGAAATAGCATTCAGGTGTCCAACTTCCTTCCTGCTG 1018
DB 838 ttttttaagtctacggtctggagaggaatcagatcgaggtctcccaacccttcttactg 897
QY 1019 GATCCGATCAAGATCGACGCTACTTTGGGCTTTCAAGTTTCAGGATAGACTGA 1075
DB 898 gatccgagcaggtgcaacatactttggggtcttttaagtttcgagatatagattga 954

Search completed: December 28, 2000, 19:38:01
Job time: 6736 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 28, 2000, 17:40:57 ; Search time 147.31 Seconds
(without alignments)
2249.467 Million cell updates/sec

Title: US-08-989-362-1
Perfect score: 2191
Sequence: 1 GCCAGGACCTCTGTGAACG.....TTTGGTACTTAAATGCG 2191

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 262060 seqs, 75620496 residues

Total number of hits satisfying chosen parameters: 524120

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, NA: *
1: /cgn2_6/ptodata/2/ina/5A-COMB.seq: *
2: /cgn2_6/ptodata/2/ina/5B-COMB.seq: *
3: /cgn2_6/ptodata/2/ina/5C-COMB.seq: *
4: /cgn2_6/ptodata/2/ina/5D-COMB.seq: *
5: /cgn2_6/ptodata/2/ina/6-COMB.seq: *
6: /cgn2_6/ptodata/2/ina/PCTUS-COMB.seq: *
7: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2144.8	97.9	2295	3	US-08-842-842-6
2	1615.8	73.7	1630	5	US-08-996-139-10
3	666.2	30.4	954	5	US-08-996-139-10
4	58.4	2.7	1042	5	US-08-584-031-2
5	58.4	2.7	1042	5	US-08-780-496-2
6	58.4	2.7	1521	2	US-08-670-354-3
7	58.4	2.7	1521	6	PCT-US96-10895-3
8	58.4	2.7	1751	2	US-08-670-354-1
9	58.4	2.7	1751	6	PCT-US96-10895-1
10	54	2.5	1366	6	PCT-US96-10895-5
11	54	2.5	1366	6	PCT-US96-10895-5
12	51.4	2.3	8220	4	US-08-568-459A-11
13	51.4	2.3	8220	4	US-08-487-826B-11
14	51.4	2.3	19124	4	US-08-487-826B-13
15	45.8	2.1	19124	4	US-08-487-826B-13
16	44.4	2.0	4257	3	US-08-690-473-1
17	44.4	2.0	12001	2	US-08-458-568A-11
18	43.4	2.0	4616	2	US-08-340-203A-1
19	43.4	2.0	4616	3	US-08-452-567-1
20	43.4	2.0	4616	4	US-08-452-427-1
21	43.4	2.0	4616	5	US-09-085-407-1
22	43.4	2.0	6243	4	US-09-056-075-1
23	42.4	1.9	2960	5	US-08-913-842-3
24	42.4	1.9	8920	3	US-08-446-855A-1
25	42	1.9	5117	5	US-08-854-585-1
26	42	1.9	5117	6	PCT-US95-05512-1

c 27	41.4	1.9	6768	2	US-08-107-755A-1	Sequence 1, Appli
c 28	41.4	1.9	8457	1	US-07-991-867B-1	Sequence 1, Appli
c 29	41.4	1.9	8457	4	US-08-544-332-1	Sequence 1, Appli
c 30	41	1.9	991	5	US-08-924-747-25	Sequence 25, Appli
c 31	40.8	1.9	2015	5	US-08-633-993A-30	Sequence 30, Appli
c 32	40.6	1.9	1120	5	US-09-030-613-1	Sequence 1, Appli
c 33	40.4	1.8	1422	2	US-08-319-704-5	Sequence 5, Appli
c 34	40.4	1.8	3095	7	5231168-1	Patent No. 5231168
c 35	40.2	1.8	2621	4	US-08-553-619B-8	Sequence 8, Appli
c 36	40.2	1.8	2897	4	US-08-927-394-1	Sequence 1, Appli
c 37	40.2	1.8	5852	1	US-07-867-106-2	Sequence 2, Appli
c 38	40.2	1.8	246240	3	US-08-724-394A-20	Sequence 20, Appli
c 39	40.2	1.8	246240	3	US-08-724-394A-21	Sequence 21, Appli
c 40	40.2	1.8	246240	3	US-08-724-394A-22	Sequence 22, Appli
c 41	40	1.8	2070	2	US-08-486-342-1	Sequence 1, Appli
c 42	40	1.8	2070	2	US-08-473-092-1	Sequence 1, Appli
c 43	40	1.8	2070	2	US-08-614-801A-1	Sequence 1, Appli
c 44	40	1.8	2076	2	US-08-066-371-1	Sequence 1, Appli
c 45	40	1.8	2076	6	PCT-US94-05666-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-842-842-6
; Sequence 6, Application US/08842842
; Patent No. 5843678
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: OSTEOCALCIN BINDING PROTEINS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91230-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,842
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-451
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2295 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 158..1105
US-08-842-842-6

Query Match	97.9%	Score 2144.8	DB 3	Length 2295
Best Local Similarity	99.4%	Pred. No. 0		
Matches 2174	Conservative 0	Mismatches 12	Indels 2	Gaps 2
Qy	1	GCAGGACCTCTGTGAACCGTGGGGGGCGCGCTGGCGGGGACTCTGCTCGCGG	60	
Db	34	GCAGGACCTCTGTGAACCGTGGGGGGCGCGCTGGCGGGGACTCTGCTCGCGG	93	
Qy	61	TGGGTGGCGGAGGAGAGAGAACGATCGGGAGCGGCGGCGGCGGCGCGG	120	

[illegible]

RESULT 2
US-08-996-139-10

[illegible]

Db 1200 TCTAACCCCTGGGACATGTGCCACTGAGA(CCTTGAANAATAAGAGATGCCATGTCTATTC 1259
QY 1449 AAACAAATGATAGTGTGAAGGGTTAAGT'CTTTTGAATTTTACATTCGCGTGGGACCTG 1508
Db 1260 AAACAAATGATAGTGTGAAGGGTTAAGT'CTTTTGAATTTTACATTCGCGTGGGACCTG 1319
QY 1509 CAATAGATTTCTTTTCTTAATGAGGA;AGAAAAATATATGATATTTTATATATGCT 1568
Db 1320 CAATAGATTTCTTTTCTTAATGAGGA;AGAAAAATATATGATATTTTATATATGCT 1379
QY 1569 AAAGTTATATTTCCAGSGTGAATGTTTC'GTGCAAAAGTTTGTAAATATATATTTGTGCTA 1628
Db 1380 AAAGTTATATTTCCAGSGTGAATGTTTC'GTGCAAAAGTTTGTAAATATATATTTGTGCTA 1439
QY 1629 TAGTATTTGATTTCAAAATATTTAAATATTTCTCACTCTTGACATATTTAAATTTTAAAT 1688
Db 1440 TAGTATTTGATTTCAAAATATTTAAATATTTCTCACTCTTGACATATTTAAATTTTAAAT 1499
QY 1689 GTACAGATGATTTAACTGTGTGACACTTTTAAATTCCTCTGAAGGTACTCGTAGCTAAGGG 1748
Db 1500 GTACAGATGATTTAACTGTGTGACACTTTTAAATTCCTCTGAAGGTACTCGTAGCTAAGGG 1559
QY 1749 GGCAGATATCTGTTCTGTTGGTGACACATTTAGTTTATTTCTTTTATTTCTTTTAACTTAAAT 1808
Db 1560 GGCAGATATCTGTTCTGTTGGTGACACATTTAGTTTATTTCTTTTATTTCTTTTAACTTAAAT 1619
QY 1809 AGACTCTTTTCAAG 1819
Db 1620 AGACTCTTTTCAAG 1630

RESULT 3
US-08-996-139-12
; Sequence 12, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/061,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/811,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644

; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 954'base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: huRANKL (full length)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..951
; US-08-996-139-12

Query Match 30.4%; Score 666.2; DB 5; Length 954;
Best Local Similarity 82.5%; Pred. No. 2e-153;
Matches 790; Conservative 0; Mismatches 158; Indels 9; Gaps 2;
QY 125 ATGCGCGGGCCAGCCGAGACTACGGCAAGTACCTGCGCAGCTCGGAGGAGATGGGCAGC 184
Db 1 ATGCGCGCGCCAGCAGAGACTACACCAAGTACCTGCGTGGCTCGGAGGAGATGGCGGC 60
QY 185 GGCCCGGCGTCCACACAGAGGTCCGCTGCACCCCGCGCTTCGCACCGGCTCCGGCG 244
Db 61 GGCCCGGAGCCCGCAGGCGCCCTGCACGCCCGCGC---CGCGCGCTCGCGCGCAC 117
QY 245 CGCCACCGCGCGCTCCCGCTCCATGTTCTGCGCCCTCTCGGGCTGGGACTGGGCCAG 304
Db 118 CAGCCCGCGCGCTCCCGCTCCATGTTCTGTTGGCCCTCTCGGGCTGGGCCAG 177
QY 305 GTGCTCTGCAGCATCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 364
Db 178 GTTGTCTGCAGCGTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 237
QY 365 TCAGAAGACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 424
Db 238 TCAGAAGATGGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 297
QY 425 CAGGACTCGACTCTGGAGAGTGAAGACAC-----ACTACCTGACTCTCTGACGAGGATG 478
Db 298 CAAGACACACTCTGGAGAGTCAAGATACAAAAATTAATACCTGATTCATGTAGGAGAATT 357
QY 479 AAACAAGCCTTTTCAGGGGCGGTGCGAGAGGAAGTGAACACATTTGTTGGGGCCACAGCGC 538
Db 358 AAACAGGCGCTTTCAAGGAGCTGTGCAAAAGGAATTTACAACATATCTGTTGGATCACAGC 417
QY 539 TTCTCAGGAGCTCCAGCTTATGATGAAGGCTCATGTTTGGATGTTGGCCAGGAGCAAG 598
Db 418 ATCAGAGCAGAGAAAGCGATGTTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 477
QY 599 CCTGAGGCGCCAGCCATTTTGACACCTCACCATCAATGCTGCCAGCATCCCATCGGTTTCC 658
Db 478 CTTGAAGCTCAGCCCTTTTGTCTCATCTCATCTATTAATGCGCAGCATCCCATCTGGTTCC 537
QY 659 CATAAAGTCACTCTGCTCTTGTGTACACGATCGAGGCTGGGCCAAGATCTCTAACATG 718
Db 538 CATAAAGTGAAGTCTGCTCTTGTGTACCATGATCGGGCTGGGCCAAGATCTTCCAACTG 597
QY 719 ACGTTAAGCAACGGAATAAGGTTAAACCAAGATGCTTCTATTTACTGTACCCCAAC 778
Db 598 ACTTTTAGCAATGGAATAACTAATAGTTAATCAGGATGCTTTTATAGCTGTATGCCAAC 657
QY 779 ATTTGCTTTTCGGCATCATGAACATCGGGAAGCGGTACCTACAGACTATCTTCAGCTGATG 838
Db 658 ATTTGCTTTTCGACATCATGAACCTTCAGGAGACCTAGCTACAGAGTATCTTCAACTAATG 717
QY 839 GTGTATGTCTGTAAACACGAGCATCAAAATCCCAAGTTCTCATACCTGNTGAAGAGGG 898

Db 718 GTGTACGTCACATAAACACGAGATCAAAATCCCAAGTCTCATACCTGATGAAGAGGA 777
QY 899 AGCAGCAAAACTGGTCGGGCAATCTCAATVCCACTTTTATTCATAAATGTTGGGGA 958
Db 778 AGCACCAGATATTGTCAGGGAATCTCAATVCCACTTTTATTCATAAACGTTGGTGA 837
QY 959 TTTTTCAGCTCCGAGCTGGTGAAGAAATAGCATTAGGTCGTCACACCTTCCTGCTG 1018
Db 838 TTTTAAAGTTACGCTGGAGAGAAATACGATCGAGGTCTCAACCCCTCTTACTG 897
QY 1019 GATCCGATCAAGATCGACGCTACTTTGGGCTTTTCAAGTTTCAGGACATAGACTGA 1075
Db 898 GATCCGATCAGGATGCACATACCTTTGGGCTTTTAAAGTTTCGAGATATAGATTGA 954

RESULT 4
US-08-584-031-2
; Sequence 2, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669,22US03
; CURRENT APPLICATION NUMBER: US/08/584,031A
; CURRENT FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1042
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-584-031-2

Query Match 2.7%; Score 58.4; DB 5; Length 1042;
Best Local Similarity 50.0%; Pred. No. 3.4e-05;
Matches 174; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

QY 713 AACATGCTGTATGCTTAAACACGAGATCAAAATCCCAAGTCTCATACCTGATGAA 892
Db 586 aactgcacttgaggaatggaactggtcatccatgaaaggggtttactacatctat 645
QY 773 GCCAACAATTTGCTTGGCATCATGAACATCGGGAGCGTACCTACAGACTATCTTCAG 832
Db 646 tcccaacatacttctgattcaggaggaa---ataaagaaacacacaaagacacaa 702
QY 833 CTGATGCTGTATGCTTAAACACGAGATCAAAATCCCAAGTCTCATACCTGATGAA 892
Db 703 caaatggtccatatttacaataacacaaagtattcccgacctatattgtgatgaa 762
QY 893 GGAGGAGCAGCAAAACTGGTCGGGCAATTTCTGAATTCCTCAATTTTCCATAAATGTT 952
Db 763 agtgcagaataatgttggctcaagatgcagaataatggaactctatccatctatcaa 822
QY 953 GGGGGATTTTCAAGCTCCGAGCTGGTGAGAAATAGCATTAGGTCGTCACACCTTCC 1012
Db 823 gggggaataattgagcttaaggaaatgacagaaatttttctctgtaacaaatgagcac 882
QY 1013 CTGCTGATCCGATCAGATCGACGCTACTTTGGGCTTTTCAAGTT 1060
Db 883 ttgatagacatggaccatgaagccagtttttctcgggccttttagtt 930

RESULT 5
US-08-780-496-2
; Sequence 2, Application US/08780496
; Patent No. 6046048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
; TITLE OF INVENTION: APO-2 Ligand
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,496
; FILING DATE: 08-Jan-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0978P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5416
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1042 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
US-08-780-496-2

Query Match 2.7%; Score 58.4; DB 5; Length 1042;
Best Local Similarity 50.0%; Pred. No. 3.4e-05;
Matches 174; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

QY 713 ACATGACGCTTAAGCAACGGAAACTAAGGGTTAACCAAGATGGCTTCTATTACTGTAC 772
Db 586 AACTTCACCTTGGAGTAATGGTGAAGTGGTTCATGCAATGAAAAAGGGTTTACTACATCTAT 645
QY 773 GCCAACAATTTGCTTGGCATCATGAACATCGGGAGCGTACCTACAGACTATCTTCAG 832
Db 646 TCCCAACATACCTTTCGATTTTCAGGAGGAA---ATAAAGAAACACACAAAGACGACAAA 702
QY 833 CTGATGCTGTATGCTTAAACACGAGATCAAAATCCCAAGTCTCATACCTGATGAAA 892
Db 703 CAAATGGTCCATATATTTACAATACACAAGTTATCTTGACCTATATTTGTTGATGAAA 762
QY 893 GGAGGAGCAGCAAAACTGGTCGGGCAATTTCTGAATTCCTCAATTTTATTCATAAATGTT 952
Db 763 AGTGCCTAGAAATAGTTGTTGGTCTAAAGATGCAGAATATGGACTCTATTCATCTATCAA 822
QY 953 GGGGGATTTTCAAGCTCCGAGCTGGTGAGAAATAGCATTAGGTCGTCACACCTTCC 1012
Db 823 GGGGGAATATTGAGCTTTAAGGAAATGACAGAAATTTTGTCTGTAACAAATGAGCAC 882
QY 1013 CTGCTGGATCCGATCAAGATCGACGCTACTTTGGGCTTTTCAAGTT 1060
Db 883 TTGATAGACATGACCATGAAGCCAGTTTTCGGGGCCTTTTAGTT 930

RESULT 6
US-08-670-354-3
; Sequence 3, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street

QY	893	GGAGGAGCACCAGAAACCTGGTCGGGCAATTTCTGAAATTCACCTTTTATTTCCATAAATGTT	952
Db	602	ACTGCTAGAAATAGTTGGTGTCTAAGATGCAGAAATGAGACTCTATTCCATCTATCAA	661
QY	953	GGGGGATTTTTCAAGCTCCGAGCTGGTCAGAAATATAGCATTCAGGTTGCCAACCCCTTC	1012
Db	662	GGGGGAATTTTACGCTTAAGGAAATGACAGATTTTGTGTTCTGTACAAATGAGCAC	721
QY	1013	CTGCTGGATCCGGATCAAGATGCGAGTACTTTGGGGCTTTTCAAAGTT	1060
Db	722	TTGATAGACATGGACCATGAAGCCAGTTTTTTTCGGGGCTTTTTTAGTT	769

RESULT 8
US-08-670-354-1
; Sequence 1, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1751 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: huAIC
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 88..933
US-08-670-354-1

Query Match 2.7%; Score 58.4; DB 2; Length 1751;

Best Local Similarity	50.08;	Pred. No.	4.4e-05;
Matches	174;	Conservative	0; Mismatches 171; Indels 3; Gaps 1;

QY	713	AACATGACGTTAAAGCAACGGAAAACTAAGGCGTTAACCAAGATGGCTTCTATTACTGTGAC	772
Db	583	AACVTGCACCTTGAGGAATGGTGAACCTGCTCATCCATGAAAAGGGTTTTACTATCATCTAT	642
QY	773	GCCAACAATTTGCTTTTCGGCATACTATGAACAACATCGGGAGCGTACCACAGACTATCTTCAG	832
Db	643	TCCCAAACATACTTTTCGATTTTCAGGAGGAA---ATAAAGAAGAAACACAAAGACGACAAA	699
QY	833	CTGATGGTGATATGCTTTAAACACGAGCATCAAAATCCCCAAGTTCTCATAACTGATGAAA	892
Db	700	CAAAATGGTCCAAATATATTTACAAATACACAAGTTATCCTGACCCCTATATTTGTTGATGAAA	759
QY	893	GGAGGGAGCAGGAAAACTGGTCGGGCAATTTCTGAATTCACACTTTTATTCATAAATGTT	952
Db	760	AGTCTAGAAATAGTTTGGTCTTAAGAGATGCCAATATGGACACTATTCATCATCTATCAA	819
QY	953	GGGGGATTTTTCACAGCTCCGAGCTGGTGAAGAAATTAGCATTCAGGTGTCCAAACCTTCC	1012
Db	820	GGGGGAATATTGAGCTTAAGGAAAAATCACAGAATTTTTGTTCTGTAACAAAATGAGCAC	879
QY	1013	CTGCTGATCGGATCAAGATGCGACGTACTTTTGGGGCTTTTCAAAGTT	1060
Db	880	TTGATAGACATGGACCATGAAGCCAGTTTTTTTCGGGGCCCTTTTATGTT	927


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RESULT      9
PCT-US96-10895-1
; Sequence 1, Application PCT/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1751 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
    
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; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: huAIC
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 88..933
; PCT-US96-10895-1

Query Match          2.7%; Score: 58.4; DB 6; Length 1751;
Best Local Similarity 50.0%; Pred No. 4.4e-05;
Matches 174; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

QY 713 AACATGACGTTAAGCAACGGAACAACTAAGTGGTTAAACCAAGATGGCTTCTATTACCTGTAC 772
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 583 AACTTCGCACTTGAGGAATGGTGAACCTGGTCAATCCATGAAAGGGTTTACTACATCTAT 642

QY 773 GCCAACAATTTGCTTTCCGGATCATGAAGAACATCGGGGAAGCGTACCTACAGACTATCTTCAG 832
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 643 TCCCAACAATACCTTTCGATTTTCAGGAGG/A---ATAAAGAAACACAAAGAACGACAAA 699

QY 833 CTGATGCTGTATCTCGTTAAACCCACACATCAAAATCCCAAGTTCTCATACCTGATGAAA 892
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 700 CAATGGTCCATATATTTACAAATACAAAGTTATCTCTGACCCCTATATTTGTTGATGAAA 759

QY 893 GGAGGAGCAGCAGAAACAACTGGTGGGCA/TTCTGAATTCACACTTTTATTCCATAAATGTT 952
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 760 AGTGCTAGAATAAGTTTGGTCTAAG/TGCAGAAATATGGAGCTCTATTTCCATCTATCAA 819

QY 953 GGGGGGATTTTCAAGTCCGAGCTGGTG/AGAAATTTAGCATTCAGGTGCCAACCCCTTCC 1012
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 820 GGGGGAATATTTGAGCTTAAGGAAATATG/CAGAAATTTTGTCTCTGTAACAATGAGCAC 879

QY 1013 CTGCTGGATCCGGATCAAGATCGGAGTTCCTTTGGGGCTTTCAAAGTT 1060
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 880 TTGATAGACATGGACCATGAAGCCAGTTTTTTGGGGGCTTTTATTAGTT 927

RESULT 10
US-08-670-354-5
; Sequence 5, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,612
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,358
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1366 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: MUAIC
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 47..919
; US-08-670-354-5

Query Match          2.5%; Score 54; DB 2; Length 1366;
Best Local Similarity 51.7%; Pred. No. 0.00046;
Matches 123; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 831 AGCTGATGGTGTATGTCTTAAACACCAGCATCAAAAATCCCAAGTTCTCATAACTGATGA 890
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 687 AACAGCTGGTGCAGTACATCTACAAGTACACACGCTATCCGGATCCCATAGTGTCTCATGA 746

QY 891 AAGGAGGGAGCAGAAACAACTGGTGGGCAATCTCGAATTCACACTTTTATTCATAAATG 950
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 747 AGAGCCGCCAGAAACAGCTGTTGGTCCAGAGATGCCGAGTACGGACTGTACTCTCATATC 806

QY 951 TTGGGGGATTTTCAAGCTCCGAGCTGGTGAAGAAATTAGCATTCAGGTGCCAACCCCTT 1010
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 807 AGGAGGATTTTTCGAGCTAAACAAAATGACAGGATTTTGTCTGTGACAATGAAC 866

QY 1011 CCTGCTGGATCCGGATCAAGATCGGAGCTACTTTGGGGCTTTTCAAAGTTTCAGGACAT 1068
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 867 ATTTGATGGACCTGGATCAAGAGCCAGCTCTTTTGGAGCCTTTTAAATTAACATAAT 924

RESULT 11
PCT-US96-10895-5
; Sequence 5, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
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RESULT 15
US-08-487-826B-13/c
: Sequence 13, Application US/08487826B
: Patent No. 5993827
: GENERAL INFORMATION:
: APPLICANT: Sim, Kim L.
: APPLICANT: Chitnis, Chetan
: APPLICANT: Miller, Louis H.
: APPLICANT: Peterson, David S.
: APPLICANT: Su, Xin-zhaun
: APPLICANT: Wellens, Thomas E.
: TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
: TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Knobbe Martens Olson & Bear
: STREET: 620 Newport Center Drive 16th Floor
: CITY: Newport Beach

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OM nucleic - nucleic search, using sw model
Run on: December 28, 2000, 09:56:08 ; Search time 1101.46 Seconds
(without alignments)
12298.703 Million cell updates/sec

Title: US-08-989-362-1
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Scoring table: IDENTITY_NUC
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Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2:*
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51: em_esthum9:*
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53: em_esthum11:*
54: em_esthum12:*
55: em_esthum13:*
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116: em_gss5:

Query Match 11.6%; Score 255.2; DB 28; Length 313;
Best Local Similarity 92.1%; Pred. No. 5.5e-48;
Matches 280; Conservative 0; Mismatches 23; Indels 1; Gaps 1;
QY 1885 AGGATGTTGGTCAACAGGTCCTTTCAAAATTTAGAGCTAATGACTTTAGGAGCTGACA 1944
DB 1 AGAGTGTGTTTCAACAGGTCCTTTCAATATTTGAAGCTAATTTGAGCTTTAGGAGCTGAGA 60
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DB 61 TACCCAAAAGGATACATAATAGGCTACTG-AAATCTTTCCAGGAGTATTTATGCAATAT 119
QY 2005 TGAACAGGTGCTTTTTTTTACAAGAGCTACAAAATGTAATTTGTTCTTTTTTTTCCC 2064
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QY 2125 TTATTTTATTTACTGTACAATAAAAGCATTTGTTCTGAATGGCATTTTGTGACTTAA 2184
DB 240 TTATTTTATTTACTGTACAATAAAAGCATTTGTTCTGAATGTTAATTTTGTGACAAA 299
QY 2185 AAAT 2188
DB 300 AAAT 303

RESULT 5
A0417854
LOCUS
DEFINITION
QY 11-185M9.TV RPCI-11 Homo sapiens genomic clone RPCI-11-185M9,
DNA sequence.
ACCESSION
VERSION
QY 117854.1 GI:4475697
KEYWORDS
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 575)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
J.C.

TITLE
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
JOURNAL
COMMENT
Unpublished (1997)
Other_GSSs: RPCI-11-185M9.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbeetigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from
Research Genet cs (inforesgen.com). BAC end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: 77
Class: BAC ends.
Location/Qualifiers
1..575
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/db_xref="GDB:757092"
/db_xref="taxon:9606"
/clone="RPCI-11-185M9"
/clone_lib="RPCI-11"
/sex="Male"

FEATURES
source

/cell_type="Lymphocytes"
/note="Vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
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Best Local Similarity 77.9%; Pred. No. 1e-47;
Matches 403; Conservative 0; Mismatches 88; Indels 26; Gaps 7;
QY 1386 GGGTCTAACCCCTGACATGTGCCACTGGAACCTTGAATTAAGAGATGCCATCTCAT 1445
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QY 1446 TSCAAAGAAATGATAGTCTGAAGGGTTAAGTTCTTTTGAATTTGTTACATTTGCCCTGGGAC 1505
DB 137 CGCAATGAAGGATCATCTGAAGGGGCAAAATCTTTTGAATTTGTTACATCATGCTGGAAC 196
QY 1506 CTGCAATAAGTCTTTTTTTTCTAATGAGGAGAGAAAATATATATGTTATTTATATAATG 1565
DB 197 CTGCAAAAAA---TACTTTTTCTAATGAGGAG-AAAATATATATGTTATTTATATAATA 252
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DB 253 TCTAAGTTATATTTTCAGATGTAATGTTTCTTTCGCAAGATTTGTAATTTATATTTG 312
QY 1626 CTATAGTATTTGATTCAAAATATTTTAAATATGTCACATGTTGACATATTTAATGTTTAA 1685
DB 313 CTATAGTATTTGATTCAAAATATTTTAAATATGTCGTTGACATATTTAATGTTTAA 372
QY 1686 AATGTACAGATGTAATTTAACTGGTGCACATTTGTAATTTCCCTG-----AAGGTACTCGTA 1740
DB 373 AATGTACAGACATATTTAACTGGTGCACATTTGTAATTTCCCTGGGAAACATTTGCAGCTA 432
QY 1741 GCTAAGGGGAGAAATATCTGTTTCTGGTGACCAATGATGTTATTTCTTTATCTTTT 1800
DB 433 AGGAGGGGAAAAAATGTTGTTTCTCTAATATCAAAATGCAATATTTCTTCTTCTTTT 492
QY 1801 AACTTAATAGA-GTCTTCAGACTTGTCAAACTATGTCAGCAAAATAAATAAATAAAT 1959
DB 493 AAGTTAATAGATTTTTTTCAGACTTGTCAAGCTGTGC-----AAAATAATT 538
QY 1860 AAAATGAATATCTTTGAATAATAAGTAGGATGTTGGTCT 1896
DB 539 AAAATGGATGCTTGAATAATAAGCAGGATGTTGGCC 575

RESULT 6
BB240334
LOCUS
DEFINITION
QY 306 bp mRNA EST 05-JUL-2000
BB240334 RIKEN full-length enriched, 3 days neonate thymus Mus
musculus cDNA clone A630081K02 3' similar to AF019048 Mus musculus
receptor activator of nuclear factor kappa B ligand (RANKL) mRNA,
mRNA sequence.
ACCESSION
VERSION
QY 306 bp mRNA EST 05-JUL-2000
BB240334
KEYWORDS
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 306)
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata
Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,
Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya
T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I.

Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al.)
Unpublished (2000)

TITLE
JOURNAL
COMMENT

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URL: http://genome.rtc.riken.go.jp/

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermotabilization and the reactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsuina,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

FEATURES
Source
1..306
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A630081K02"
/clone_lib="RIKEN full-length enriched, 3 days neonate
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/dev_stage="3 days neonate"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATCTCGAGTTAATTAATATCCCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I."

BASE COUNT 104 a 50 c 38 g 114 t
ORIGIN

Query Match 11.5%; Score 251.6; DB 28; Length 306;
Best Local Similarity 93.2%; Pred. No. 3.6e-47;
Matches 274; Conservative 0; M1.matches 19; Indels 1; Gaps 1;

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Db 4 TCACCAGTCCCTTCAATTTAGAGCTATTGACTTTGAGAGTGACACCCAAAAA 63
QY 1955 GGATACATAATAGGCTACTGAAATCTGTAGGAGTATTATGCAATTTTGAACAGGTG 2014
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Db 64 GGATACATAATAGGCTACTG-AAAATCTGTGAGGATATTATTCCAATTTTGAACAGGTG 122
QY 2015 TCTTTTTTTTACAGAGCTACAAATTTGTAAATTTTCTTTCTTTTCTCCCATAGAAAAATG 2074
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QY 2135 ATACTGTACAAATAAAGCATTTGTTCTGAATGGCATTTTTTTGGTACTTAAAAAT 2188
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Db 243 ATACTGTACAAATAAAGCATTTGTTCTGAATTTTGGTACTACAAAAAT 296

RESULT 7
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LOCUS BB223942 RIKEN full-length enriched, adult male aorta and vein Mus
DEFINITION musculus cDNA clone A530084G16 3' similar to AF019048 Mus musculus
receptor activator of nuclear factor kappa B ligand (RANKL) mRNA,
mRNA sequence.
BB223942
BB223942.1 GI:8892554

ACCESSION
VERSION BB223942
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 317)

REFERENCE
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.,
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y.,
Shigenoto,Y., Shinagawa,A., Shiraki,T., Sobabe,Y., Sugahara,Y.,
Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.,
Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al.)
Unpublished (2000)

TITLE Yoshihide Hayashizaki
JOURNAL Genome Exploration Research Group, Life Science Tsukuba Center,
COMMENT Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
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Fax: +81-298-36-9098
Email: genome-res@rtc.riken.go.jp/
URL: http://genome.rtc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermotabilization and the reactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsuina,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

Location/Qualifiers
1..317
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A530084G16"
/clone_lib="RIKEN full-length enriched, adult male aorta
and vein"

FEATURES
Source
1..317
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A530084G16"
/clone_lib="RIKEN full-length enriched, adult male aorta
and vein"

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1954	QY	AGGATACATAATAGGTACTGAAAATCTGTCAAGAGTATTTATGCAATTTTGAACAGGT	2013
64	Db	AGGATACATAATAGGTACTGTG-ACATCCGTCAAGAGTATTTATGCAATTTTGAACAGGT	122

, Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toyota,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiaki,A., Yoshino,M., Muramatsu,M. and Hayashizaki.Y.
RIKEN mouse ESTs (Konno.H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@rtc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

Location/Qualifiers
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/clone_lib="A630056P18"
/cdna_lib="RIKEN full-length enriched, 3 days neonate thymus"
/tissue_type="thymus"
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/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAAGGATCAAGACTCTTTTCTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAATTCTCGATTAAATAATTCCTCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

108 a 57 c 37 g 114 t
Ch 10.8%; Score 236.6; DB 28; Length 316;
Similarity 89.8%; Pred.No.9.6e-44;
165; Conservative 0; Mismatches 29; Indels 1; Gaps 1;
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CCACCTGCCCTTTCAAATTTAGAAACAATCAACTTAGCAGCTCACATACCCAANA 63
GGATACATAATAGGCTACTGAAAATCTGTCCAGGAGTATTTATGCAATTTATGAACAGGT 2013
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Db 183 GTAATATAGTTTATACGCAAAAAACAA'CCACTTTTAAATTTAGTGAAGATTTATTTAT 242
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QY 2134 TATAGTGTACATAAAGCAATGTTTCT'AAATGGCAATTTTGGTACTTAAAAAT 2188
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RESULT 9
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LOCUS HS 5256.B2.G09.T7A.RPCI-11 Human Male BAC Library Homo sapiens
DEFINITION genomic clone Plate-832 Co.-18 Row=N, DNA sequence.
ACCESSION A0827168
VERSION A0827168.1 GI:5793230
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 529)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Research Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 832 row: N column: 18
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Class: BAC ends
High quality sequence stop: 529.
FEATURES
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and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBA3.6 vector at EcoRI sites"
BASE COUNT 147 a 121 c 102 g 153 t 6 others
ORIGIN
Query Match 10.5%; Score 229; DB 103; Length 529;
Best Local Similarity 72.9%; Pred. No. 5,7e-42;
Matches 336; Conservative 0; Mismatches 114; Indels 11; Gaps 3;

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QY 924 CTGAATTCACATTTTATTTCCATAAATGTTGGGAGATTTTTCAGAGTCGAGCTGTGAAG 983
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Db 407 CTGAATTCACATTTTATTTCCATAAACGTTGGTGATTTTGTAAAGTTAGGGTCTGGAGAG 348
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 984 AAATTACATTCAGGTGTCCAAACCTTCCCTGCTGGATCCGATCAAGATCGGAGTACT 1043
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 347 AAATCAGCATCGAGGTCTCCAAACCTTCCCTTACTGGATCCGATCAGGATCAACATACT 288
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1044 TTGGGGCTTTCAAGTTTCAGGACATAGACTAGACTCATTTTCGTGGACATATTAGCATGA 1103
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 287 TTGGGGCTTTTAAAGTTTCGAGATATAGATTGAGCCCGAGTTTTCGAGTGT---ATGTA 231
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1104 TGTCTTAGATGTTTGGAAACTTCTTAAAAA-----ATGGATGATGCTTATACATGTGT 1156
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 230 TCTCTGTGATGTTTGGAAACATTTTANACAGCCCAAGAAAGATGTATATAGGTGTGT 171
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1157 AGACTACTAAGACATGCGCCACAGGTGTATGAAATTCACAGCCCTCTCTCTTGAAGCTT 1216
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 170 GAGACTACTAAGAGCATGCGCCCAACGGTACACGACTCAGTATCCATGCTCTTGAACCTT 111
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QY 1217 GTACAGGTGCTGTATATGTAAGTCCATAGGTGATGTTAGATTCATGGTG-ATTACACAA 1275
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Db 110 GTAGAACACAGCATGTTTACAGCCAGTGGGAGATGTAGACTCATGCTGTGTTACACAA 51
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QY 1276 CGGTTTACAAATTTGTAATGATTTCCTAAGAAATTGAACCA 1316
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Db 50 TGGTTTGTAGATTTGTAGNAGTACTACGACTGCAACAA 10
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RESULT 10
BB216722 288 bp mRNA EST 30-JUN-2000
LOCUS BB216722 RIKEN full-length enriched, adult male aorta and vein Mus
DEFINITION musculus cDNA clone A530038L03 3' similar to AF019048 Mus musculus
receptor activator of nuclear factor kappa B ligand (RANKL) mRNA,
mRNA sequence.
ACCESSION BB216722
VERSION BB216722.1 GI:8881675
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 288)
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.,
Matsuyama,T., Mikita,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.,
Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomimaga,N., Toya
T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.,
Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno,H., et al.)
Unpublished (2000)
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URL:http://genome.rtc.riken.go.jp/
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
```


trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsuunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y., and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

Source

1..288
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A530038L03"
/clone_lib="RIKEN full-length enriched, adult male aorta and vein"
/sex="male"
/tissue_type="aorta and vein"
/dev_stage="adult"
/lab_host="DH10B"
/note="Site.1: Sali; Site.2: BamHI: cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAATTAATTAATTCCTCCCTCCCTCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

BASE COUNT 96 a 42 c 42 g 108 t

ORIGIN

Query Match 10.3%; Score 225.6; DB 28; Length 288;
Best Local Similarity 92.5%; Pred. No. 3.1e-41;
Matches 259; Conservative 0; Mismatches 19; Indels 2; Gaps 2;
QY 1909 TCAATTTAGAACCTAATTCAGCTTTAGGAGCTGACATAGCCAAAGGATACATAATAGG 1968
Db 1 TCATATTTAGAGCTAATTCAGCTTTAGGAGCTGACATACCCAGG-AGGATACATAATAGC 59
QY 1969 CTACTGAAATCTGTCAGGAGTATTATGCAATATTGACAGGTGCTTTTTTACAAG 2028
Db 60 CTACTG-CAATCTGTCAGGAGTATTATGCAATATTGTCAGAGGTGCTTTTTTACAAG 118
QY 2029 AGCTACAAATTTGAAATTTTGTCTTTTTCCTCCATAGAAAATGACTATGTTTATC 2088
Db 119 AGCTACAAATTTGAAATTTTGTCTTTTTCCTCCATAGAACATGACTATGTTTATC 178
QY 2089 AGCCAAAACAAATCCACATTTTAAATTTAGTGAAGTTATTTTATTACTGTACAATAA 2148
Db 179 AGCCAAAACAAATCCACATTTTAAATTTAGTGAAGTTATTTTATTATATGTCACATAA 238
QY 2149 AGCATTTGTTCTGAATGGCATTTTGTGGTACTTAAAT 2188
Db 239 AAGCATTTGTTCTGAATGGTAAATTTTGTGGTACTTAAAT 278

RESULT 11

BB236016
LOCUS BB236016 314 bp mRNA EST 05-JUL-2000
DEFINITION BB236016 RIKEN full-length enriched, 3 days neonate thymus Mus

musculus cDNA clone A630056006 3' similar to AF019048 Mus musculus receptor activator of nuclear factor kappa B ligand (RANKL) mRNA, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BB236016
GI:8917884

EST

house mouse

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 314)

REFERENCE

AUTHORS

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arai, A., Hayatsu, N., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Itoh, M., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Konno, H., et al.)
Unpublished (2000)

TITLE

JOURNAL

COMMENT

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Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermotranscription and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsuunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
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FEATURES

Source

1..314
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A630056006"
/clone_lib="RIKEN full-length enriched, 3 days neonate thymus"
/tissue_type="thymus"
/dev_stage="3 days neonate"
/lab_host="DH10B"
/note="Site.1: Sali; Site.2: BamHI: cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTCTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of

sequence [5' GAGA:AGAGATTCTCGAGTTAATTAATAATCCCGCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I."

BASE COUNT 103 a 64 c 39 j 108 t
ORIGIN

Query Match 10.0%; Score: 219.8; DB 28; Length 314;
Best Local Similarity 88.5%; Pred. No. 6.5e-40;
Matches 261; Conservative 0; M.smatches 32; Indels 2; Gaps 2;

QY 1895 TCACCAGGTGCTTCAAAATTTAGAGGCTAATTGACTTTAGGAGCTGACATAGCCAAAAA 1954
Db 3 TCACCAGTTCCTTTTCCACTTACATCTAGAAGC:AATCGACTTTAGGAGCTGACATAGCCGAAA 62
QY 1955 GGATACATATAGGCTACTGAAATCTG:CAGGAGTATTTATGCAATTTATGAACAGGTG 2014
Db 63 GGATACATACAGGCTACTG-AAATCTC:CAGGAGCATTTATCCAAATTTATGAACAGGTG 121
QY 2015 TCCTTT-TTTTACAAGAGCTACAAATTTCTTAAATTTGTTCTTTTTCCTCATAGAAAAAT 2073
Db 122 TCCTTTCTCCACAAGAGCTACAAATTTGT:AATTTGTCTTTTTCCTCATAGGAAAT 181
QY 2074 GTACTATAGTTATACGCCAAAAACAACACCTTTTAAATTTAGTGAAGTTATTTAT 2133
Db 182 GTACTATACCTTATCAGCCCAAAACAACACCTTTTAAATTTAGTGAAGTTATTTAT 241
QY 2134 TATACGTACAAATAAAGAGATCTTCTCAATGCGATTTTTCGTACTTAAAAAT 2188
Db 242 TATACGTACTATAAAGAGATCTCTCTCAATGTTAATTTTGGTACAAAAAAT 296

RESULT 12

BB229867

LOCUS

DEFINITION BB229867 RIKEN full-length enriched, 3 days neonate thymus Mus
musculus cDNA clone A630024A04 3' similar to AF019048 Mus musculus
receptor activator of nuclear factor kappa B ligand (RANKL) mRNA,
mRNA sequence.

ACCESSION BB229867

VERSION BB229867.1

KEYWORDS GI:8900512

SOURCE EST.

ORGANISM house mouse.

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 282)

REFERENCE
AUTHORS Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
Hirozane,T., Hori,F., Ishii Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Izawa,M., Kadota,K., Kagawa I., Kai,C., Kawai,J., Kikuchi,N.,
Kiyosawa,H., Kojima,Y., Komio,S., Koya,S., Kurihara,C., Kusakabe,M.,
Matsuyama,T., Miki,R., Miuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
Y., Shigenoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.,
Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.,
Yano,K., Yasunishi,A., Yohota,T., Yoshida,K., Yoshiki,A., Yoshino
M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno.H., et al.)
Unpublished (2000)

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URL: http://genome.rtc.riken.go.jp/

Carninci,P., Nishiyama,Y., Vestover,A., Itoh,M., Nagaoka,S., Sasaki

. . .

FEATURES

SOURCE

1..282
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="A630024A04"
/clone_lib="RIKEN full-length enriched, 3 days neonate
thymus"
/tissue_type="thymus"
/dev_stage="3 days neonate"
/lab_host="DH10B"
/notes="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAAGGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 20.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCGAGTTAATAATATCCCGCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I."

BASE COUNT 94 a 44 c 36 g 108 t

ORIGIN

Query Match 9.7%; Score 211.6; DB 28; Length 282;
Best Local Similarity 90.5%; Pred. No. 4.8e-38;
Matches 248; Conservative 0; Mismatches 24; Indels 2; Gaps 2;

QY 1915 TTAGAAGCTAATTGACCTTAGGAGCTGACATAGCCAAAAGGATACATAATAGGCTACTG 1974

Db 1 TTTGAATCTAATTGAC-CTACGTGCTGACATACCCCAAAAGGTTACATAATAGGCTACTG 59

QY 1975 AAAATCTGTCAGGAGTATTTATGCAATTTATGAACAGGTGCTTTTTTTTACAAGAGCTAC 2034

Db 60 AG-ATCTGTCAGGAGTATTTATGCAATTTATGAACAGGTGCTTTTTTTTACAAGAGCTAC 118

QY 2035 AAATTTGTAATTTTGTGTTCTTTTTTTTCCCATAGAAATGTACTATAGTTTATCAGCCAA 2094

Db 119 AAATTTGTAATTTTGTGTTCTTTTTTTTCCCATAGAAATGTACTATAGTTTATCAGCCAA 178

QY 2095 AAACAATCCACTTTTTTAATTTAGTGAAGTATTTTATTTACTGTACAATAAAGCAT 2154

Db 179 AAACAATCCACTTTTTTAATTTAGTGAAGTATTTTATTTACTGTACAATAAAGCAT 238

QY 2155 TGTTCCTGAATGGCATTTTTTTTGGTACTTAAAAAT 2188

Db 239 TGCTCTGAAATCTTAATTTTTTGGTACAAAAAT 272

RESULT 13

BB234550

LOCUS

BB234550 277 bp mRNA EST 04-JUL-2000

DEFINITION
 BB234550 RIKEN full-length enriched, 3 days neonate thymus Mus musculus cDNA clone A630049P08 3' similar to AF019048 Mus musculus receptor activator of nuclear factor kappa B ligand (RANKL) mRNA, mRNA sequence.

ACCESSION
 BB234550
VERSION
 BB234550.1 GI:8914405
KEYWORDS
 EST.
SOURCE
 mouse.
ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 277)

REFERENCE
AUTHORS
 Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,K., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigenoto,Y., Shingawa,A., Shiraki,T., Soabe,Y., Sugahara,I., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tomimaga,N., Toyota,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
 RIKEN Mouse ESTs (Konno,H., et al.)
 Unpublished (2000)

TITLE
 RIKEN full-length enriched, 3 days neonate thymus cDNA
JOURNAL
 Genomic Exploration Research Group, Life Science Tsukuba Center,
 Genome Science Laboratory
COMMENT
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 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
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 Fax: +81-298-36-9098
 Email: genome-res@rtc.riken.go.jp,
 URL:http://genome.rtc.riken.go.jp/
 Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
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 Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
 Carninci,P. and Hayashizaki,Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES
 Location/Qualifiers
 1..277
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="A630049P08"
 /clone_lib="RIKEN full-length enriched, 3 days neonate thymus"
 /tissue_type="thymus"
 /dev_stage="3 days neonate"
 /lab_host="DH10B"
 /note="Site_1: Sali; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer 15'
 GAGAGAGAAGGATCCAGAGCTCTTTTCTTTTCTTTTCTTNN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0 Second

strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATTCTCGAGTTAAATTAATCCGCCCCCCC					
3']. cDNA was cleaved with xhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from lambda					
FLC I."					
BASE COUNT	96 a	49 c	30 g	102 t	
ORIGIN					
Query Match	9.2%; Score 200.6; DB 28; Length 277;				
Best Local Similarity	88.4%; Pred. No. 1.5e-35;				
Matches 229; Conservative	0; Mismatches 29; Indels 1; Gaps 1;				
QY 1930 CTTTAGGAGCTGACATAGACCACAAAAGGATCATATAATAGGTACTGAGAAATCTGTCAAGAG 1989					
Db 1 CTTTCGCACCCGAATACCCCAAAGCATACATTATTGGCTFACTG-AAATCTATCAGGAC 59					
QY 1990 TATTATGCAATTATTGAACAGAGTGCTCTTTTTTACAAGAGCTACAAATGTGAATTTTG 2049					
Db 60 TATTATGCAATTATTGAACAGAGCTGCTTTTTTTCACAAAGAGCTACAAATGTGAATTTTG 119					
QY 2050 TTTCCTTTTTTCCCATTAGAAAAATGTACTATAGTTTATFACGCCAAAAAACAATCCACTTT 2109					
Db 120 TTTCCTTTTTTCCCATTAGAAAAATGTACTATAGTTTATFACGCCAAAAAACAATCCACTTT 179					
QY 2110 TTAATTTAGTGAAGTTTATTTTATTATCTGTACATAAAGAAGCTGTTCTCTGAATGGCA 2169					
Db 180 TTAATTTAGTGAAGTTTATTTTATTATCTGTACATAAAGAAGCTGTTCTCTGAATGGTA 239					
QY 2170 TTTTTTGGTACTTAAAAAT 2188					
Db 240 ATTTTTTGGTACAAAAAT 258					
RESULT 14					
BB236026					
LOCUS	BB236026	316 bp	mRNA	EST	04-JUL-2000
DEFINITION	musculus cDNA clone A630056P12 3' similar to AF019048 Mus musculus receptor activator of nuclear factor kappa B ligand (RANKL) mRNA, mRNA sequence.				
ACCESSION	BB236026				
VERSION	BB236026.1 GI:8915651				
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci K., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Itazawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya,T., Tsunoda,Y., Watabiki,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.				
TITLE	RIKEN Mouse ESTs (Konno,H., et al.)				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Yoshihide Hayashizaki Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Tel: +81-298-36-9013 Fax: +81-298-36-9098 Email: genome-res@rtc.riken.go.jp/ URL:http://genome.rtc.riken.go.jp/				

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Katsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

Source

Location/Qualifiers
1. .316
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A630056P1."
/tissue="thymus"
/dev_stage="3 day: neonate"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
GAGAGAGAGAGCTCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAAATTAATCCCTCCCTCCCTCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

BASE COUNT 104 a 68 c 33 g 111 t

ORIGIN

Query Match 8.9%; Score 195; DB 28; Length 316;
Best Local Similarity 86.8%; Pred. No. 3e-34;
Matches 249; Conservative 0; M.matches 35; Indels 3; Gaps 3;
QY 1903 TGCCTTTCAAAATTTAGAGCTAATGACTTTAGGAGCTGACATAGCCAAAAGGATACAT 1962
Db 14 TCCCTTTCTAATCTTGAACCAATGACTTA-CAGCCACATACCTAAAGGATACCT 72
QY 1963 AATAGCTACTGAAATCTGTGAGAGTA:TTATGCAATTTTGACAGGTGTCCTTT-TT 2021
Db 73 CATAGGCCACTG-AAATCTGTGAGGAGTA:TTATCAATTTACTGAACGCGCTCTTCTT 131
QY 2022 TTACAAGAGCTACAAATTTGTAATTTTGTTCCTTTTTTCCATAGAAAATGCTACTATA 2081
Db 132 CTACAGAGCTACAAATTTGTAATTTATTCCTTTTTTCCATAGAAAATGCTACTATA 191
QY 2082 GTTTATGACCCAAAACCAATCCACTTTTAAATTTAGTGAAGTTATTTATTTACTGT 2141
Db 192 GTCTATACCCAAAACCAATCCACTTTTAAATTTAGTGAAGTTATTTATTTACTGT 251
QY 2142 ACAATAAAGCAATTTTCTGATGCAATTTTGTGATCTTAAAT 2188
Db 252 ACAATAAAGCAATTTCTCTGATGTTAAATTTTGTGATCAAAAAAT 298

RESULT 15

AV315022

..

LOCUS DEFINITION

AV315022 251 bp mRNA EST 08-NOV-1999
cDNA clone 5830427E05 3' similar to AF019048 Mus musculus receptor activator of nuclear factor kappa B ligand (RANKL) mRNA, mRNA sequence.

ACCESSION

AV315022

VERSION

AV315022.1

KEYWORDS

Source

ORGANISM

Mus musculus

REFERENCE

Authors

TITLE

Journal

COMMENT

Contact: Yoshihide Hayashizaki

Genome Exploration Research Group, Life Science Tsukuba Center,

Genome Science Laboratory

The Institute of Physical and Chemical Research (RIKEN), Genomic

Sciences Center

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan

Tel: +81-298-36-9013

Fax: +81-298-36-9098

Email: genome-res@rtc.riken.go.jp

URL: <http://genome.rtc.riken.go.jp/>

Sasaki,M., Izawa,M., Watanishi,M., Ozawa,K., Tanaka,T., Yoneda,Y.,

Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki

,Y.

Transcriptional sequencing: A method for DNA sequencing using RNA

polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)

Itoh,M., Katsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,

Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki

,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation

system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303,

19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for

further details.

Location/Qualifiers

1. .251

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="5830427E05"

/clone_lib="RIKEN full-length enriched, adult male thymus"

/sex="male"

/tissue_type="thymus"

/dev_stage="adult"

/lab_host="DH10B"

/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'
GAGAGAGAGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second

FEATURES

Source

strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGATTCTCGAGTTAATTAATCCCCCCCCCC
3']. cDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
BamHI."

BASE COUNT 84 a 35 c 31 g 101 t
ORIGIN

Query Match 8.6%; Score 187.4; DB 17; Length 251;
Best Local Similarity 92.5%; Pred. No. 1.6e-32;
Matches 197; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 1976 AAATCTGTCAGGAGTATTTATGCAATATTGAACAGGTGCTTTTACAAAGAGCTACA 2035
Db 20 AAATCTGTCAGGAGTATTTATCGACTATTGAACAGGTATCTTTTACAAAGAGCTACA 79
QY 2036 AATTGTAAATTTGTTCTTTTTCCTCCCATAGAAAATGCTACTATAGTTTATCAGCCAAA 2095
Db 80 AATTGTAAATTTGTTCTTTTTCCTCCCATAGAAAATGCTACTATAGTTTATCAGCCAAA 139
QY 2096 AAACAATCCACTTTTAAATTTAGTGAAGTTATTATTACTGTACATAAAAGCAT 2155
Db 140 AAACAATCCACTTTTAAATTTGTTGAAGTTATTATTACTGTACATAAAAGCAT 199
QY 2156 GTTCTGTAATGGCATTTTGGTACTTAAAAAT 2188
Db 200 TTTTCTGAATGTTAATTTTGGTACAAAAAT 232

Search completed: December 28, 2000, 18:03:43
Job time:: 29255 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 28, 2000, 18:03:46 ; Search time 61.2 Seconds
(without alignments)
176.556 Million cell updates/sec

Title: US-08-989-362-2
Perfect score: 1675
Sequence: 1 MRRASRDYGYKLRSEEMGS.....LLDPDQDATYGFAPKVQDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq.36.*
1: /cgn2_2/gcgdata/geneseq/geneseqp/AA1980.DAT.*
2: /cgn2_2/gcgdata/geneseq/geneseqp/AA1981.DAT.*
3: /cgn2_2/gcgdata/geneseq/geneseqp/AA1982.DAT.*
4: /cgn2_2/gcgdata/geneseq/geneseqp/AA1983.DAT.*
5: /cgn2_2/gcgdata/geneseq/geneseqp/AA1984.DAT.*
6: /cgn2_2/gcgdata/geneseq/geneseqp/AA1985.DAT.*
7: /cgn2_2/gcgdata/geneseq/geneseqp/AA1986.DAT.*
8: /cgn2_2/gcgdata/geneseq/geneseqp/AA1987.DAT.*
9: /cgn2_2/gcgdata/geneseq/geneseqp/AA1988.DAT.*
10: /cgn2_2/gcgdata/geneseq/geneseqp/AA1989.DAT.*
11: /cgn2_2/gcgdata/geneseq/geneseqp/AA1990.DAT.*
12: /cgn2_2/gcgdata/geneseq/geneseqp/AA1991.DAT.*
13: /cgn2_2/gcgdata/geneseq/geneseqp/AA1992.DAT.*
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21: /cgn2_2/gcgdata/geneseq/geneseqp/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1675	100.0	316	19 W83194	Human osteoprotege
2	1675	100.0	316	19 W83017	Osteoclastogenesis
3	1675	100.0	316	19 W59654	Amino acid sequenc
4	1675	100.0	316	20 Y17874	Murine TRANCE. Mu
5	1675	100.0	316	21 Y84418	Amino acid sequenc
6	1675	100.0	316	21 Y84419	Amino acid sequenc
7	1554	92.8	294	19 W69956	NF-kB receptor act
8	1554	92.8	294	19 W68292	NF-kB receptor act
9	1417.5	84.6	317	19 W83195	Human osteoprotege
10	1417.5	84.6	317	19 W69957	NF-kB receptor act
11	1417.5	84.6	317	19 W68293	NF-kB receptor act
12	1417.5	84.6	317	21 Y84417	Amino acid sequenc

13	1409.5	84.1	317	19 W83018	Osteoclastogenesis
14	1297	77.4	244	19 W83019	A murine OCIF-bind
15	1107	66.1	246	19 W83020	Osteoclastogenesis
16	1101	65.7	245	20 Y17873	Human TRANCE. Hom
17	852	50.9	173	21 Y84421	Amino acid sequenc
18	852	50.9	187	21 Y84420	Amino acid sequenc
19	842	50.3	173	21 Y84422	A murine osteoprot
20	804.5	48.0	188	21 Y84423	An osteoprotegerin
21	794.5	47.4	182	21 Y84424	An osteoprotegerin
22	771	46.0	173	21 Y84425	DNA encoding osteo
23	732	43.7	173	21 Y84426	An osteoprotegerin
24	259.5	15.5	281	20 Y27016	Human Apo-2 ligand
25	259.5	15.5	281	20 Y27017	Human Apo-2 ligand
26	258.5	15.4	279	19 W76332	Human TL2 (TRAIL),
27	258.5	15.4	279	20 W95032	Tumour necrosis fa
28	258.5	15.4	281	18 W27134	Human Apoptosis in
29	258.5	15.4	281	18 W19787	Human Apoptosis in
30	258.5	15.4	281	18 W19777	Novel cytokine Apo
31	258.5	15.4	281	19 W76829	Human TL2 protein.
32	258.5	15.4	281	19 W56760	Human TRAIL polype
33	258.5	15.4	281	19 W44354	Human AGP-1. Homo
34	258.5	15.4	281	20 Y27012	Human Apo-2 ligand
35	258.5	15.4	281	20 Y01517	Protein associated
36	258.5	15.4	281	21 Y81956	Human Apo-2 ligand
37	252.5	15.1	281	20 Y27019	Human Apo-2 ligand
38	251.5	15.0	281	20 Y01516	Protein associated
39	250.5	15.0	281	20 Y27018	Human Apo-2 ligand
40	244	14.6	291	18 W19788	Mouse apoptosis in
41	244	14.6	291	19 W56762	Murine TRAIL polyp
42	244	14.6	291	19 W44353	Murine AGP-1. Mus
43	183	10.9	278	16 R79095	Rat Fas ligand enc
44	183	10.9	278	20 W98069	Rat Fas ligand (fa
45	183	10.9	278	20 W95040	Rat FasL protein.

ALIGNMENTS

RESULT 1

W83194 ID W83194 standard; Protein; 316 AA.
XX W83194;
AC W83194;
XX
DT 11-FEB-1999 (first entry)
XX
DE Human osteoprotegerin binding protein from the 32D-F3 ins.

XX Human; osteoprotegerin binding protein; OPG binding protein; arthritis;
KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
KW hypercalcaemia; osteoclast differentiation and activation and activation receptor;
KW Paget's disease.
XX
XX Homo sapiens.
OS
XX W09846751-A1.
PN
XX
XX 22-OCT-1998.
PD
XX
XX 15-APR-1998; 98WO-US07584.
PF
XX
XX 30-MAR-1998; 98US-0052521.
PR
XX 16-APR-1997; 97US-0842842.
PR
XX 23-JUN-1997; 97US-0880855.
XX
XX (AMGE-) AMGEN INC.
PA
XX Boyle WJ;
PI
XX WPI: 1998-594578/50.
XX
XX N-PSDB; W70284.
XX
XX Nucleic acid encoding osteoprotegerin binding protein - useful for,


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RESULT 3
ID W59654 standard; Protein; 316 AA.
XX AC W59654;
XX 24-SEP-1998 (first entry)
XX Amino acid sequence of mouse 499E9 protein.
DE Mouse 499E9 protein; polarised Th1 T cell; immune cell; apoptosis;
KW antagonist; autoimmune disorder; rheumatoid arthritis;
KW systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis;
XX acute inflammatory response; antibody; antigen; cancer.
XX Mus sp.
XX Key Location/Qualifiers
FT Domain 1..49
FT /note= "intracellular domain"
FT Domain 70..316
FT /note= "extracellular domain"
XX W09825958-A2.
XX 18-JUN-1998.
XX 12-DEC-1997; 97WO-US222766.
XX 13-DEC-1996; 96US-0032846.
XX (SCHE ) SCHERING CORP.
XX Gorman DM, Mattison JD;
XX WPI; 1998-348452/30.
XX N-PSDB; V41489.
XX Mouse cell surface antigen, 499E9 protein - used to treat conditions
XX associated with abnormal physiology or development
XX Claim 1; Pages 8-11; 59pp; English.
XX This is the amino acid sequence of the mouse 499E9 protein, used
XX in the method of the invention to treat conditions associated with
XX abnormal physiology or development. The 499E9 protein is expressed
XX highly on polarised Th1 T cells. Binding of 499E9 to its receptor may
XX result in either immune cell expansion or apoptosis. Antagonists of
XX 499E9 may be used to modulate immune responses in abnormal situations,
XX e.g. autoimmune disorders including rheumatoid arthritis, systemic
XX lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well as
XX acute inflammatory responses in which T-cell expansion, activation or
XX immunological T-cell memory play an important role. The antibodies
XX can be used to raise anti-idiotypic antibodies which will be useful
XX in detecting or diagnosing various immunological conditions related to
XX the expression of antigens of 499E9. The antibodies, and fragments of
XX 499E9 can be used in the treatment of conditions associated with
XX abnormal physiology or development, including abnormal proliferation
XX (e.g. cancerous conditions) or degenerative conditions.
XX Sequence 316 AA;
Query Match 100.0%; Score 1675; DB 19; Length 316;
Best Local Similarity 100.0%; Pred. No. 6.4e-144;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRRASRDYGYLRSEDMGSGVPHBEGPLHPAPSAPAPPPAASRSMFLALLGLGQ 60
DB 1 mrrasrdygykylrsseemsgvgphbgplhpapsapapppaasrsmflallglgq 60
QY 61 VVCSIALFLYFRAQMDPNRISDSTHCFYRILRLHENAGLQDSTLESFDTLPDSCRMKQ 120
|||||

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Db 61 vvczialflyfraqmdpnrisdsthcfyrlrlhenagldstlesedtlpdscrmkq 120
QY 121 AFQGAVKELQHIYGPQRFSGAPAMWEGSWLDVAGRGKPEAQPFPAHLTTNAASIPSGSHK 180
|||||
Db 121 afqgavqkelghivgqrfsgapammegswldvagrkgpeaqpfahltnaasipsgshk 180
XX 181 VTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICF8HHFTSGSVPTDYLOLMVY 240
|||||
Db 181 vtlsswyhdrgwaklsnmtlsngklrvnqdgfyylyanlcf8hhtsgsvptdylolmvy 240
QY 241 VVKTSIKIPSSHNLMKGGSTKNWGNSEFHYFINVGGFFKLRAGEEISIQVSNP5LLDP 300
|||||
Db 241 vvktsikipsshnlmkggstknwgnsefhyfinvggffkkrageeisivsnp5lldp 300
QY 301 DQDATYFGAFKVDID 316
Db 301 dqdatyfgafkvqdid 316
RESULT 4
Y17874
ID Y17874 standard; Protein; 316 AA.
XX AC Y17874;
XX 17-AUG-1999 (first entry)
XX Murine TRANCE.
XX TRANCE; tumour necrosis factor superfamily; signal transduction; TNF;
XX TNF-related activation induced cytokine; immune response; cancer;
XX autoimmune disease; HIV; hypersensitivity; allergen.
XX Mus musculus.
XX W09929865-A2.
XX 17-JUN-1999.
XX 14-DEC-1998; 98WO-US26486.
XX 11-DEC-1998; 98US-0989479.
XX 12-DEC-1997; 97US-0989479.
XX 03-MAR-1998; 98US-0034099.
XX (UVRQ ) UNIV ROCKEFELLER.
XX Choi Y, Josien R, Steinman R, Won B;
XX WPI; 1999-385609/32.
XX N-PSDB; X80224.
XX TNF like proteins for treating autoimmunity and cancer
XX Claim 9; Fig 3; 164pp; English.
XX The present sequence represents murine TNF-related activation induced
XX cytokines (TRANCE). Human or murine TRANCE polypeptides or their
XX variants, fragments, derivatives or analogues may be used as modulators
XX of immune response in a mammal comprising, antisense sequences to
XX TRANCE and fusion proteins comprising human and/or murine TRANCE.
XX Agonists and antagonists of TRANCE, can be used to modulate immune
XX response by increasing or decreasing the life span of mature dendritic
XX cells and increasing or decreasing T cell activation. These techniques
XX are especially useful for treating immune system related conditions such
XX as HIV, cancer, autoimmune disease or hypersensitivity to an allergen.
XX The TRANCE polypeptides can be used to increase the viability of
XX dendritic cells in vivo or in vitro, especially when used in conjunction
XX with proteins of the tumour necrosis factor (TNF) superfamily (especially
XX CD40L or TNF-alpha).
XX Sequence 316 AA;

```


QY 143 PAMMEGSLDVAQRCKPEAQPFALHTINLASIPSGSHKVTLSWYHRCWAKISNMTLSN 202
 Db 121 pammeqswldvaqrckpeaqpfahltin:asipsgshkvtlswwyhrdwakismntlsn 180
 QY 203 GKLRVNQDGFYLYANICFRHETSGSVTDYLOLMVYVVKTSIKIPSSHNLMKGGSTKN 262
 Db 181 gklrvnqdgfylyanicfrhetskgsvtqlylmvyvvtksikipsshnlmkgsstkn 240
 QY 263 WSGNSEFHYSINVGFFKLKRAAGEEISIQVSNPSSLDPDQDATYFGAFKVDID 316
 Db 241 wsgnsefhysinvgffklrageeisi:qvsnpslldpdqdatyfgafkvqid 294

RESULT 8

W68292
 ID W68292 standard; Protein: 294 AA.

AC W68292;

XX 08-OCT-1998 (first entry)

DE NF-kB receptor activator RANK ligand (RANKL).

XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 KW immune response; inflammatory response; toxic shock; sepsis;
 KW RANKL; RANK ligand; tumour necrosis factor; TNF; mouse.

XX Mus musculus.

XX W09828424-A2.

PD 02-JUL-1998.

XX 22-DEC-1997; 97WO-US23866.

XX 14-OCT-1997; 97US-0064671.

PR 23-DEC-1996; 96US-0059978.

PR 07-MAR-1997; 97US-0813509.

XX (IMMV) IMMUNEX CORP.

XX Anderson DM, Galibert LJ, Marashovsky E;

XX WPI: 1998-377655/32.

DR N-PSDB; V41371.

XX New isolated receptor activator of necrosis factor-kappa B - useful
 PT for, e.g. developing products for regulating an immune or
 PT inflammatory response, treating toxic shock or sepsis

XX Example 7: Pages 55-57; 80pp; English.

XX This represents a murine RANKL, a ligand for the RANK (receptor
 CC activator of necrosis factor-kappa B (NF-kB)) polypeptide. RANK is a
 CC member of the tumour necrosis factor (TNF) family. Host cells transformed
 CC or transfected with an expression vector comprising the RANK encoding
 CC nucleic acid can be used to produce recombinant RANK protein. The soluble
 CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to
 CC RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
 CC used for regulating an immune or inflammatory response. Inhibition of
 CC NF-kB by RANK antagonists may be useful in ameliorating negative effects
 CC of an inflammatory response that result from triggering of RANK, e.g. in
 CC treating toxic shock or sepsis, graft-versus-host reactions, or acute
 CC inflammatory reactions. They can also be used in adjunct therapy for
 CC disease characterised by neoplastic cells that express RANK. The products
 CC can also be used for detection and drug screening.

XX Sequence 294 AA;

Query Match 92.8%; Score 1554; DB 19; Length 294;

50 55

Best Local Similarity 99.7%; Pred. No. 5.3e-133;
 Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GVPEHGLHPAPAPAPPPAASRSRMFLALLGLGLGVVCSIALFLYFRQAMPNRISE 82
 Db 1 gvpehglhpapapppaasrsrmflalilgilgvvcsialflyfrqampnriise 60

QY 83 DSTHCFYRILRLHENAGLQDSTLSEDTLPDSCRMRKQAFQGVOKELQHIIVGPQRFSGA 142
 Db 61 dsthcfyrlrlhenadlqdstlesedtlpdscrmrkqafgavqkelqhlivgqprfsga 120

QY 143 PAMMEGSLDVAQRCKPEAQPFALHTINLASIPSGSHKVTLSWYHRCWAKISNMTLSN 202
 Db 121 pammeqswldvaqrckpeaqpfahltinaasipsgshkvtlswwyhrdwakismntlsn 180

QY 203 GKLRVNQDGFYLYANICFRHETSGSVTDYLOLMVYVVKTSIKIPSSHNLMKGGSTKN 262
 Db 181 gklrvnqdgfylyanicfrhetskgsvtqlylmvyvvtksikipsshnlmkgsstkn 240

QY 263 WSGNSEFHYSINVGFFKLKRAAGEEISIQVSNPSSLDPDQDATYFGAFKVDID 316
 Db 241 wsgnsefhysinvgffklrageeisi:qvsnpslldpdqdatyfgafkvqid 294

RESULT 9

W83195
 ID W83195 standard; Protein: 317 AA.

AC W83195;

XX 11-FEB-1999 (first entry)

DE Human osteoprotegerin binding protein from the pcDNA/huOPGbp1.linsert.
 KW Human; osteoprotegerin binding protein; OPG binding protein; arthritis;
 KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODA;
 KW hypercalcaemia; osteoclast differentiation and activation receptor;
 XX Paget's disease.
 XX Homo sapiens.
 XX W09846751-A1.
 XX 22-OCT-1998.
 XX 15-APR-1998; 98WO-US07584.
 XX 30-MAR-1998; 98US-0052521.
 PR 16-APR-1997; 97US-0842842.
 PR 23-JUN-1997; 97US-0880855.
 XX (AMGE-) AMGEN INC.
 XX Boyle WJ;
 XX WPI: 1998-594578/50.
 DR N-PSDB; V70285.

XX Nucleic acid encoding osteoprotegerin binding protein - useful for,
 PT e.g. treating bone diseases by modulating osteoclast differentiation
 PT and for diagnosis

XX Claim 19; Fig 4; 47pp; English.

XX The present sequence is human osteoprotegerin (OPG) binding protein.
 CC Host cells transfected with vectors containing nucleic acid molecules
 CC encoding OPG binding protein are used to produce recombinant OPG binding
 CC protein. OPG binding protein is used in binding assays to determine
 CC osteoprotegerin (OPG) in biological samples; to screen for specific
 CC binding agents (particularly agonists and antagonists, including
 CC intracellular proteins); to raise Ab (useful in immunoassays for
 CC detection of OPG binding protein) and to identify compounds that
 CC modulate binding of OPG binding protein to osteoclast differentiation

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OM protein - protein search, using sw model

Run on: December 28, 2000, 18:48:36 ; Search time 157.95 Seconds
(without alignments)
33.533 Million cell updates/sec

Title: US-08-989-362-2
Perfect score: 1675
Sequence: 1 MRRASRDYGYKLSRSEMG.....LLDPQDATYGFQVQDID 316

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/prodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/2/iaa/6_COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6CTUS_COMB.pep.*
5: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1675	100.0	316	2	US-08-842-842-7
2	1554	92.8	294	3	US-08-996-139-11
3	1417.5	84.6	317	3	US-08-996-139-13
4	258.5	15.4	281	1	US-08-670-354-2
5	258.5	15.4	281	3	US-08-584-031-1
6	258.5	15.4	281	3	US-08-780-496-1
7	258.5	15.4	281	4	PCT-US96-10895-2
8	244	14.6	291	1	US-08-670-354-6
9	244	14.6	291	1	PCT-US96-10895-6
10	173.5	10.4	281	2	US-08-810-453-2
11	173.5	10.4	281	3	US-08-815-190A-2
12	173.5	10.4	281	4	PCT-US95-00362-2
13	171.5	10.2	261	1	US-07-940-605A-2
14	171.5	10.2	261	1	US-08-184-422-8
15	171.5	10.2	261	1	US-08-360-923A-2
16	171.5	10.2	261	1	US-08-446-922-4
17	171.5	10.2	261	2	US-08-431-055-4
18	171.5	10.2	261	2	US-08-690-096-2
19	171.5	10.2	261	2	US-08-249-189-12
20	171.5	10.2	261	2	US-08-484-624A-12
21	171.5	10.2	261	2	US-08-477-733B-12
22	171.5	10.2	261	3	US-08-763-995-2
23	171.5	10.2	261	3	US-09-088-913A-12
24	171.5	10.2	261	3	US-08-589-771B-8
25	171.5	10.2	261	4	PCT-US93-10034-4
26	169	10.1	279	4	PCT-US95-00362-5
27	160	9.6	473	2	US-08-249-189-16
28	160	9.6	473	2	US-08-484-624A-16

29	160	9.6	473	2	US-08-477-733B-16	Sequence 16, Appl
30	160	9.6	473	3	US-09-088-913A-16	Sequence 16, Appl
31	159	9.5	273	1	US-08-446-922-11	Sequence 11, Appl
32	159	9.5	273	2	US-08-249-189-21	Sequence 21, Appl
33	159	9.5	273	2	US-08-484-624A-21	Sequence 21, Appl
34	159	9.5	273	2	US-08-477-733B-21	Sequence 21, Appl
35	159	9.5	273	3	US-09-088-913A-21	Sequence 21, Appl
36	157	9.4	260	1	US-08-446-922-6	Sequence 6, Appl
37	157	9.4	260	2	US-08-431-055-2	Sequence 2, Appl
38	157	9.4	260	2	US-08-249-189-2	Sequence 2, Appl
39	157	9.4	260	2	US-08-484-624A-2	Sequence 2, Appl
40	157	9.4	260	2	US-08-477-733B-2	Sequence 2, Appl
41	157	9.4	260	3	US-09-088-913A-2	Sequence 2, Appl
42	157	9.4	260	4	PCT-US93-10034-6	Sequence 6, Appl
43	154	9.2	151	1	US-07-940-605A-3	Sequence 3, Appl
44	154	9.2	151	2	US-08-690-096-3	Sequence 3, Appl
45	152	9.1	149	3	US-08-584-031-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-842-842-7
; Sequence 7, Application US/08842842
; Patent No. 5843678
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; TITLE OF INVENTION: OSTEOPROTEGERIN BINDING PROTEINS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91230-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,842
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-451
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-842-842-7

Query Match 100.0%; Score 1675; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 2.2e-157;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MRRASRDYGYKLSRSEMGSGVPEHGLHPAPAPAPPPAASRSMFLALLGLGLQ	60
Db	1	MRRASRDYGYKLSRSEMGSGVPEHGLHPAPAPAPPPAASRSMFLALLGLGLQ	60
QY	61	VVCSTALFLYFRAQMDPNRISDSSTHCFYRILRLHENAGLQDSTLESDTLPDSCRMKQ	120
Db	61	VVCSTALFLYFRAQMDPNRISDSSTHCFYRILRLHENAGLQDSTLESDTLPDSCRMKQ	120
QY	121	AFQGAQVQKELQHVGPQFSGAPAMMEGSLDVAQKPKPAQFPAHLLTINAASIPSGSHK	180
Db	121	AFQGAQVQKELQHVGPQFSGAPAMMEGSLDVAQKPKPAQFPAHLLTINAASIPSGSHK	180

QY 181 VTLSWYHDSRGWAKISNMTLSNCKLRVNJDGFYLYLANICFRHHETSGSVPTDYQLQVMY 240
Db 181 VTLSWYHDSRGWAKISNMTLSNCKLRVNJDGFYLYLANICFRHHETSGSVPTDYQLQVMY 240
QY 241 VVKTSIKIPSSHNLMKGGSTKNWGSNSENHFYSINVGFFKLRAGEISIOVSNPSSLLDP 300
Db 241 VVKTSIKIPSSHNLMKGGSTKNWGSNSENHFYSINVGFFKLRAGEISIOVSNPSSLLDP 300
QY 301 DQDATYFGAFKVQDID 316
Db 301 DQDATYFGAFKVQDID 316
RESULT 2
US-08-996-139-11
; Sequence 11, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/066,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/811,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/771,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-1
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 294 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-996-139-11

Query Match 92.8%; Score: 1554; DB 3; Length 294;
Best Local Similarity 99.7%; Pred. No. 1.7e-145;
Matches 293; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 23 GVPHEGLHPAPSAPAPAPPPAASRMFIALGLGLGVVCSIALFLYFRAQMDPNRISE 82
Db 1 GVPHEGLHPAPSAPAPAPPPAASRMFIALGLGLGVVCSIALFLYFRAQMDPNRISE 60

QY 83 DSTHCFYRILRLHENAGLQDSTLESDTLDPSCRRMKQAFQAVOKELQHTVGPQRFSGA 142
Db 61 DSTHCFYRILRLHENAGLQDSTLESDTLDPSCRRMKQAFQAVOKELQHTVGPQRFSGA 120
QY 143 PAMMEGSLWDAVQKGPFAHLTINAASIPSGSHKVTLLSSWYHDSRGWAKISNMTLSN 202
Db 121 PAMMEGSLWDAVQKGPFAHLTINAASIPSGSHKVTLLSSWYHDSRGWAKISNMTLSN 180
QY 203 GKLRVNDGFFYLYLANICFRHHETSGSVPTDYQLQVMYVVKTSIKIPSSHNLMKGGSTKN 262
Db 181 GKLRVNDGFFYLYLANICFRHHETSGSVPTDYQLQVMYVVKTSIKIPSSHNLMKGGSTKN 240
QY 263 WSGNSEHFYSINVGFFKLRAGEISIOVSNPSSLLDPDQDATYFGAFKVQDID 316
Db 241 WSGNSEHFYSINVGFFKLRAGEISIOVSNPSSLLDPDQDATYFGAFKVQDID 294
RESULT 3
US-08-996-139-13
; Sequence 13, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 317 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-996-139-13

Query Match 84.6%; Score 1417.5; DB 3; Length 317;
Best Local Similarity 84.3%; Pred. No. 5.5e-132;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

QY 1 MRRASRDYGYKLRSEDMGSGVPGVHPGEPHPAPAPAPPPAASRMFIALGLGLGQ 60

||||| 1 MRRASRDYKYLGRSEEMGGPAPHEGLH-APPPAPHPQPPAASRMFVALLGLGLGQ 59
QY 61 VVCSIALFLYFRAQMDPNRISEDTCHCFYRILRLHENAGLQDSTLESDT--LPDSCRRM 118
Db 60 VVCSVALFFYFRAQMDPNRISEDTCHCFYRILRLHENADFDTTLESQDTKLIPDSCRR 119
QY 119 KOAFQAVQKELQHIYVGPQFSGAPAMMEGSLWDVAQRGKPEAQPFPAHLTINAAISIPSGS 178
Db 120 KOAFQAVQKELQHIYVGSQHRAEKAWDGSWLDLAKRSLKLEAQPFPAHLTINATDIPSGS 179
QY 179 HKVTLSSWTHDRGWAKISNMTLSNGKLRVNDGFFYLYANICFRHHETSGSVPTDYQLQM 238
Db 180 HKVTLSSWTHDRGWAKISNMTLSNGKLRVNDGFFYLYANICFRHHETSGDLATEYLQLM 239
QY 239 VYVTKSIKIPSSHNLKMGSTNWSNSEFHFYSINVGFFFKLRAGEEISIQVNSPLL 298
Db 240 VYVTKSIKIPSSHNLKMGSTNWSNSEFHFYSINVGFFFKLRAGEEISIEVNSPLL 299
QY 299 DPQDATYFGAFKVDID 316
Db 300 DPQDATYFGAFKVRDID 317

RESULT 4

US-08-670-354-2
; Sequence 2, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESS: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-670-354-2

Query Match 15.4%; Score 258.5; DB 1; Length 281;
Best Local Similarity 26.4%; Pred No. 9.8e-18;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;
QY 43 PAASRMFLALLGLGLGVVCSIALFLYFRAQMD--PNRISEDTCHCFYRILRLHENAGL 100
Db 10 PSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGKIACF-----LKEDDSY 64
QY 101 QDSTLESDTLPDSCRRMKQAFQGVQK-----ELQHVGPQFSGAPAMM 146
Db 65 WDP--NDEESMNSPCQVQKWQLRVKMLRTSEETISTVQEKQONISPL----- 113
QY 147 EGSWLDVAQRGKPEAQPFPAHLT-----INAAISIPSGSHKVTL---SSWYHDR-GWAKIS 196
Db 114 -----VREGRQVRA--AHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLS 165
QY 197 NMTLSNGKLRVNDGFFYLYANICFRHHETSGSVPTDYQLQMVVYVYKTIKIPSSHNLK 256
Db 166 NLHLRNGELVIERKGFYIYSQTYFRFQEEIKENTKNDQMVQYIYKYT-SYPDPILLMK 224
QY 257 GGSTKNWSNSEFHFYSINVGFFFKLRAGEEISIQVNSPLLDPQDATYFGAFK 312
Db 225 SARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASEFFGAFLV 280

RESULT 5

US-08-584-031-1
; Sequence 1, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/08/584,031A
; CURRENT FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-584-031-1

Query Match 15.4%; Score 258.5; DB 3; Length 281;
Best Local Similarity 26.4%; Pred No. 9.8e-18;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;
QY 43 PAASRMFLALLGLGLGVVCSIALFLYFRAQMD--PNRISEDTCHCFYRILRLHENAGL 100
Db 10 PSLGQTCVLIVFTVLLQSLCAVAVTVYFTNELKQMDKYSGKIACF-----LKEDDSY 64
QY 101 QDSTLESDTLPDSCRRMKQAFQGVQK-----ELQHVGPQFSGAPAMM 146
Db 65 WDP--NDEESMNSPCQVQKWQLRVKMLRTSEETISTVQEKQONISPL----- 113
QY 147 EGSWLDVAQRGKPEAQPFPAHLT-----INAAISIPSGSHKVTL---SSWYHDR-GWAKIS 196
Db 114 -----VREGRQVRA--AHITGTRGRSNTLSSPNKNEKALGRKINSWESSRSGHSFLS 165
QY 197 NMTLSNGKLRVNDGFFYLYANICFRHHETSGSVPTDYQLQMVVYVYKTIKIPSSHNLK 256
Db 166 NLHLRNGELVIERKGFYIYSQTYFRFQEEIKENTKNDQMVQYIYKYT-SYPDPILLMK 224
QY 257 GGSTKNWSNSEFHFYSINVGFFFKLRAGEEISIQVNSPLLDPQDATYFGAFK 312
Db 225 SARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASEFFGAFLV 280

RESULT 6

US-08-780-496-1
; Sequence 1, Application US/08780496


```

1 STREET: 51 University Street
2 CITY: Seattle
3 STATE: WA
4 COUNTRY: USA
5 ZIP: 98101
6
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Floppy disk
9 COMPUTER: Apple Macintosh
10 OPERATING SYSTEM: Apple 7.5.2
11 SOFTWARE: Microsoft Word, Version 6.0.1
12
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/670,354
15 FILING DATE: 25-JUN-1996
16 CLASSIFICATION: 435
17
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 08/496,632
20 FILING DATE: 29-JUN-1995
21 CLASSIFICATION: 435
22
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US 08/548,368
25 FILING DATE: 01-NOV-1995
26 CLASSIFICATION: 435
27
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Anderson, Kathryn A.
30 REGISTRATION NUMBER: 32,172
31 REFERENCE/DOCKET NUMBER: 2835-B
32
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: (206) 587-0430
35 TELEFAX: (206) 233-0644
36 TELEX: 756822
37
38 INFORMATION FOR SEQ ID NO: 6:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 291 amino acids
41 TYPE: amino acid
42 TOPOLOGY: linear
43
44 MOLECULE TYPE: protein
45
46 US-08-670-354-6

```

Query Match 14.6%; Score 244; DB 1; Length 291;
Best Local Similarity 27.5%; Pred. NO. 2.8e-16;
Matches 83; Conservative 50; Mismatches 111; Indels 58; Gaps 15;

Qy	52	ALLGLGLGQ-----VVC5IAL-----FLYFRAQMD--PNRISESTHCFYRIL	92
Db	6	ALKDLSFSQHFRRMVICIVLLQVLLQAVSVAVTYMTNEMKQLQDNY5KIGLACFSK--	63
Qy	93	RLHENAGLDSTLSEDTLPDSC----RMMQAFQAGAVOKELOHIVG--PQRFSGNAPMM	146
Db	64	---TDEDFWDS--DGEILNRPLCQVKRQLYQLIEVTLRTFQDTISTYPEKQLSTPPLP	118
Qy	147	EGSWLDVAQKGPKEAPQFAHUT-----INAAISPGSHKVTL----SSWYHDR-GWAKTS	196
Db	119	RG-----GRFQ-KVAAHITGTRNSALPI5KDGKTKLQKTESWESRKGHSFNL	169
Qy	197	NMTLSNGKLKRVNDGFFYLYANICFRHE-----TSGSVPTDYL----OLMWVYVVKTSIKIPS	250
Db	170	HVLFRNGELVIEGLYYIYSQTYFRFQAEAD5KWK5DKVTRKQLQVYIKYTT--SYDP	228
Qy	251	SHNLMKGGSTKNN5G5NEHFHYSIVNGVGFKKLRAGEEISIQV5NPSLLDDPDQATYFGAF	310
Db	229	PIVLMKSARN5CSWR5AEYGLYSIYGGGLFELKKNDRIFV5VTNEHMLDLDQEA5FFGAF	288
Qy	311	KV	312
Db	289	LI	290

RESULT 9
PCT-US96-10895-6
; Sequence 6, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.

```

1  TITLE OF INVENTION:  Cytokine That Induces Apoptosis
2  NUMBER OF SEQUENCES:  9
3  CORRESPONDENCE ADDRESS:
4  ADDRESSEE:  Kathryn A. Anderson, Immunex Corporation
5  STREET:  51 University Street
6  CITY:  Seattle
7  STATE:  WA
8  COUNTRY:  USA
9  ZIP:  98101
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE:  Floppy disk
12 COMPUTER:  Apple Macintosh
13 OPERATING SYSTEM:  Apple 7.5.2
14 SOFTWARE:  Microsoft Word, Version 6.0.1
15 CURRENT APPLICATION NUMBER:  PCT/US96/10895
16 APPLICATION NUMBER:  PCT/US96/10895
17 FILING DATE:  25-JUN-1996
18 CLASSIFICATION:
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER:  US 08/496,632
21 FILING DATE:  29-JUN-1995
22 CLASSIFICATION:
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER:  US 08/548,368
25 FILING DATE:  01-NOV-1995
26 CLASSIFICATION:
27 ATTORNEY/AGENT INFORMATION:
28 NAME:  Anderson, Kathryn A.
29 REGISTRATION NUMBER:  32,172
30 REFERENCE/DOCKET NUMBER:  2835-WO
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE:  (206) 587-0430
33 TELEFAX:  (206) 233-0644
34 TELEX:  756822
35 INFORMATION FOR SEQ ID NO:  6:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH:  291 amino acids
38 TYPE:  amino acid
39 TOPOLOGY:  linear
40 MOLECULE TYPE:  protein
41 PCT-US96-10895-6

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Query Match 14.6%; Score 244; DB 4; Length 291;
Best Local Similarity 27.5%; Pred. NO. 2.8e-16;
Matches 83; Conservative 50; Mismatches 111; Indels 58; Gaps 15;

Qy	52	ALLGLGLGQ-----VVCSTAL-----FLYRAQMD--PNRISDESTHCFYRL	92
Dd	6	AKDLSPFSQHFRMVICIVLLQLQAQSVAVTYMYFTNEMKLOLDQNSYKIGLACFSK-	63
Qy	93	RLHENAGLDQSTLESDTLPDSC----RRMKAFQCAVOKELQIHVG---PQRFSGAPAMM	146
Dd	64	--TDDEFWDST--DGEILNRNPCLQVKRYOLQIEVTLTRTFQDTISTVPKQLSTPLP	118
Qy	147	EGSWLDVAOQRKPCEAOPFAHLT-----INAASTPSGSHKVTL-----SSWYHDR-GWAKIS	196
Dd	119	RG-----GRQP-KVAAHITGTPRSNALIPISKCKTKLCQKTESWESKRKGHSFUP	169
Qy	197	NMTLSNGKLRVNDGGYYLYANICFRHE---TSGSVPTDYL---QLMWVVYVKTSTIKIPS	250
Dd	170	HVLFRNGELVIEQGLYYIYSQTFFRFQAEADASKMVSKDKVRTKOLVOYIKYT-SYPD	228
Qy	251	SHNLMGKGTKNWSGNSEPHFYSYNVGGFPFKIRAGEEISIQVSNPSSLDDPDQDATYFGAF	310
Dd	229	PVLMKSARNCSWRDAEYGLYSIIYGGLFELKKNDRI FVSVTNEHMLDLDQEASEFFGAF	288
Qy	311	KV	312
Dd	289	LI	290

RESULT 10

US-08-810-453-2
; Sequence 2, Application US/08810453
; Patent No. 5858990
; GENERAL INFORMATION:
; APPLICANT: Walsh, Kenneth
; TITLE OF INVENTION: FAS LIGAND COMPOSITIONS FOR TREATMENT OF
; PROLIFERATIVE DISORDERS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Jacks, P.C.
; STREET: Federal Reserve Plaza, 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02210-2211
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/810,453
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Plumer, Elizabeth R.
; REGISTRATION NUMBER: 36,637
; REFERENCE/DOCKET NUMBER: S1237,7004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)720-3500
; TELEFAX: (617)720-2441
; TELEX: 343
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-810-453-2

Query Match 10.4%; Score 173.5; DB 2; Length 281;
Best Local Similarity 21.2%; Pred. No. 2.4e-09;
Matches 67; Conservative 42; Mismatches 108; Indels 99; Gaps 9;
QY 22 PGVPHGGLHPAPAPAPAPPPAASR-----SMFLALLGLGL 58
DB 40 PGQRRPPPPPPPPPPPPPPPLPLPLPLKKGHNHSTGCLLVMMFFVVLVALVGLGL 99
QY 59 GQVVCISALFLYFRAQMDPNRISESTHCFYRILRLHENAGLDQSTLESEDTLPDSCRRM 118
DB 100 G-----MFQLFHLQ-----KELAELESTSQMHTA----- 124
QY 119 KOAFQAVOKELQIHVGPORFSGAPAMMEISWLDVAQRKGPEAQPPAHLT--INAASTPS 176
DB 125 -----SSLEKQIGHPSPPPE-----KKELRKVAHLTGKSNRSMP- 159
QY 177 GSHKVTLSWYHIDRGWAKISNMTLSNGKLKRVNDQGFYLYANICFRHHTSGSVPTDYLO 236
DB 160 -----LEWEDTYGIVLLSGVKYKKGGLVINETGLFYVYSKYVFRGQSCNN-----LP 206
QY 237 LMVYVVKTSIKIPSSHNLMKGGSTKNWGNSEFHFYSINVGFFFKLRAGEEISIOVSNPS 296
DB 207 LSHKVMNRNSKYPQDLVME-KGMMSYCTTGQMMARSSYLGAVENTLSADHLYVNVSELS 265
QY 297 LLDPODATYFGAFKV 312
DB 266 LVNFESQTFGLYKL 281
RESULT 11
US-08-815-190A-2
; Sequence 2, Application US/08815190A

Patent No. 6046310
; GENERAL INFORMATION:
; APPLICANT: Queen, Cary L.
; APPLICANT: Schneider, William P.
; APPLICANT: Vasquez, Maximiliano
; TITLE OF INVENTION: Fas Ligand Fusion Proteins and Their
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/815,190A
; FILING DATE: 11-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/614,584
; FILING DATE: 13-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 011823-006710US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-815-190A-2

Query Match 10.4%; Score 173.5; DB 3; Length 281;
Best Local Similarity 21.2%; Pred. No. 2.4e-09;
Matches 67; Conservative 42; Mismatches 108; Indels 99; Gaps 9;
QY 22 PGVPHGGLHPAPAPAPAPPPAASR-----SMFLALLGLGL 58
DB 40 PGQRRPPPPPPPPPPPPPPPLPLPLPLKKGHNHSTGCLLVMMFFVVLVALVGLGL 99
QY 59 GQVVCISALFLYFRAQMDPNRISESTHCFYRILRLHENAGLDQSTLESEDTLPDSCRRM 118
DB 100 G-----MFQLFHLQ-----KELAELESTSQMHTA----- 124
QY 119 KOAFQAVOKELQIHVGPORFSGAPAMMEISWLDVAQRKGPEAQPPAHLT--INAASTPS 176
DB 125 -----SSLEKQIGHPSPPPE-----KKELRKVAHLTGKSNRSMP- 159
QY 177 GSHKVTLSWYHIDRGWAKISNMTLSNGKLKRVNDQGFYLYANICFRHHTSGSVPTDYLO 236
DB 160 -----LEWEDTYGIVLLSGVKYKKGGLVINETGLFYVYSKYVFRGQSCNN-----LP 206
QY 237 LMVYVVKTSIKIPSSHNLMKGGSTKNWGNSEFHFYSINVGFFFKLRAGEEISIOVSNPS 296
DB 207 LSHKVMNRNSKYPQDLVME-KGMMSYCTTGQMMARSSYLGAVENTLSADHLYVNVSELS 265
QY 297 LLDPODATYFGAFKV 312
DB 266 LVNFESQTFGLYKL 281
RESULT 12

RESULT 13
US-07-940-605A-2
: Sequence 2, Application US/07940605A

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Query Match      10.2%; Sequence 171.5; DB 1; Length 261;
Best Local Similarity 25.2%; Pred. No. 3.4e-09;
Matches 75; Conservative 49; Mismatches 111; Indels 63; Gaps 16;

QY 33 APSAPAPAPPAASRSMFLAILGLGLGVQVCSIALF-LYFRAQMDPNRISDSTHCFVRI 91
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 9 SPRSAATGLP--ISMKIFMYLLTVFLITQMLGSAUFAYLHRRLD--KIEDER----- 57

QY 92 LRLHE-----NAGLODSTLESDTLPDSCRRMKQAFQAGVOKELQHIIVGPORFS 140
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 58 -NLHEDFVFMKTIQRCTNGERSLSLL-----NCEETKQSEGFV-KDIM-----LN 101

QY 141 GAPAMMEGSWLDVAQRCKPEAOPPAHLTINAASIPSSGHKVTLLSSWYHDCRWAKISN--M 198
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 102 KEETKKNSEF--EMQGDQNPQIAAHV-----ISEASKTTSVLQWAEKGIYVTSMNLV 153

QY 199 TLSNGK-LRVNQDGFYLYIANICF-RHHTSGSVPTDYLOLMVYVVKTSIKIPSSHN--L 254
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 154 TLENGKQLTVKRGLYIYIAQVTFCSNREASSQAP-----FIASLCLKSPGRFERIL 205

QY 255 MKGSGSTRNWSGSEFHEYSINVGFFKLRAGEEETSIQVSNPSLLDPDODATYFGAFKV 312
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 206 LRAANTH--SSAKPCGQOSIHLGGVFELQPGASVFVNVPDPSQVSHGTFGTFFGLLKL 261

RESULT 14
US-08-184-422-8
; Sequence 8, Application US/08184422
; Patent No. 5563321
; GENERAL INFORMATION:
; APPLICANT: ARMITAGE, RICHARD
; APPLICANT: DAVISON, BARRY
; APPLICANT: FANSLAW, WILLIAM
```

APPLICANT: RENSHAW, BLAIR
APPLICANT: SPRIGGS, MELANIE
APPLICANT: WIDMER, MICHAEL
TITLE OF INVENTION: DETECTION AND TREATMENT OF MUTATIONS
TITLE OF INVENTION: IN A CD40 LIGAND GENE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Operating System 7.1
SOFTWARE: MS Word for Apple 5.1, Version a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/184,122
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/009,258
FILING DATE: 01/22/93
ATTORNEY/AGENT INFORMATION:
NAME: PERKINS, PATRICIA ANNE
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2810-A
TELEPHONE: 2065870430
TELEFAX: 2065870606
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-184-422-8

Query Match 10.2%; Score 171.5; DB 1; Length 261;
Best Local Similarity 25.2%; Pred. No. 3.4e-09;
Matches 75; Conservative 49; Mismatches 111; Indels 63; Gaps 16;
QY 33 APSAPAPAPPPAASRSMFLALLGLGQVVCISIALF-LYFRAQMDPNRISEDSTHCFYRI 91
Db 9 SPRSAATGLP--ISMKIFMYLLTVFLITMIGSALFAVYLHRRLD--KIEDER----- 57
QY 92 LRLHE-----NAGLQDSTLESEITLPDSCRRMKQAFQAVQKELQHLVGPQRF 140
Db 58 -NLHEDFVFMKTIQRCNTGERSLSLL-----NCEIKSQFEGFV-KDIM-----LN 101
QY 141 GAPAMMEGSLDVAQRKPEAQPFAHLT:NAASIPSGSHKVTLSWYHDRGWAKISN--M 198
Db 102 KEETKENSEF--EMQKGDQNPQIAAHV-----ISEASKTTTSLQWAEKGYTMSNNLV 153
QY 199 TLSNGK-LRVNODGFYLYANICF-RHHITSGSVPTDYQLQMLVYVVKTSIKIPSSHN--L 254
Db 154 TLENGKQLTVKRGQLYIYAQVTFCSNRRIASSQAP-----FIASLCLKSPGRFERIL 205
QY 255 MKGGSTKNWGSNHFHYINVGPFKLAGREISIQVSNPSSLDDPDQDATYFGAFKV 312
Db 206 LRAANTH--SSAKPCGQSIHLGGVFEL(PGASVFVNVTDPQSVSHGTGFTSGLLKL 261

RESULT 15
US-08-360-923A-2
Sequence 2, Application US/08360923A
Patent No. 5674492
GENERAL INFORMATION:
APPLICANT: ARMSTRONG, RICHARD
APPLICANT: FANSLAW, WILLIAM

APPLICANT: LONGO, DAN L.
APPLICANT: MURPHY, WILLIAM
TITLE OF INVENTION: METHOD OF PREVENTING OR TREATING
TITLE OF INVENTION: DISEASE CHARACTERIZED BY NEOPLASTIC CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMUNEX CORPORATION
STREET: 51 UNIVERSITY STREET
CITY: SEATTLE
STATE: WASHINGTON
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: Apple Macintosh System 7.1
SOFTWARE: Microsoft Word for Macintosh, Version #5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,923A
FILING DATE: December 21, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/172,664
FILING DATE: December 23, 1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2818-A
TELEPHONE: (206)587-0430
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 261 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-360-923A-2

Query Match 10.2%; Score 171.5; DB 1; Length 261;
Best Local Similarity 25.2%; Pred. No. 3.4e-09;
Matches 75; Conservative 49; Mismatches 111; Indels 63; Gaps 16;
QY 33 APSAPAPAPPPAASRSMFLALLGLGQVVCISIALF-LYFRAQMDPNRISEDSTHCFYRI 91
Db 9 SPRSAATGLP--ISMKIFMYLLTVFLITMIGSALFAVYLHRRLD--KIEDER----- 57
QY 92 LRLHE-----NAGLQDSTLESEITLPDSCRRMKQAFQAVQKELQHLVGPQRF 140
Db 58 -NLHEDFVFMKTIQRCNTGERSLSLL-----NCEIKSQFEGFV-KDIM-----LN 101
QY 141 GAPAMMEGSLDVAQRKPEAQPFAHLT:NAASIPSGSHKVTLSWYHDRGWAKISN--M 198
Db 102 KEETKENSEF--EMQKGDQNPQIAAHV-----ISEASKTTTSLQWAEKGYTMSNNLV 153
QY 199 TLSNGK-LRVNODGFYLYANICF-RHHETSGSVPTDYQLQMLVYVVKTSIKIPSSHN--L 254
Db 154 TLENGKQLTVKRGQLYIYAQVTFCSNRRIASSQAP-----FIASLCLKSPGRFERIL 205
QY 255 MKGGSTKNWGSNHFHYINVGPFKLAGREISIQVSNPSSLDDPDQDATYFGAFKV 312
Db 206 LRAANTH--SSAKPCGQSIHLGGVFEL(PGASVFVNVTDPQSVSHGTGFTSGLLKL 261

Search completed: December 29, 2000, 03:57:31
Job time: 32935 sec

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Date: Dec 29, 2000 12:16 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

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-Q/cgn2_1/USPTO.spool/US08989362/runat_28122000_095657_24324/app_query.fasta_1.377
-DB=GenEmbl -OFMT=fastap -SUFFIX=rge -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOCPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -XGAPOP=6.000
-XGAPEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500 -DELOP=6.000
-DELEX=7.000 -START=1 -MATRIX=blomsum62 -FRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE=LOCAL -OUTFT=pfs -NORM=ext -MINLEN=0
-MAXLEN=200000000 -USER=US08989362.@CGL_1.4407 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-08-989-362-2

Query length: 316

Database: GenEmbl.*

Database sequences: 1033670

Database length: -211117393

Search time (sec): 1030.300000

score_list:	Strd Orig	zScore	BScore	Len	Documentation
Sequence	+ 1675.00	2428.84	3.6e-127	951	AB008426 Mus musculus mRNA for
gb_ro:AB008426	+ 1675.00	2428.84	3.6e-127	951	AB036798 Mus musculus mRNA for
gb_ro:AB036798	+ 1675.00	2421.78	9.0e-127	2237	AF013170 Mus musculus TNF-rela
gb_ro:AF013170	+ 1675.00	2421.57	9.3e-127	2295	AF062119 Sequence 6 from paten
gb_pat:AF062119	+ 1675.00	2421.55	9.3e-127	2299	AF053713 Mus musculus osteop
gb_ro:AF053713	+ 1668.00	2411.64	3.3e-126	2225	AF019048 Mus musculus receptor
gb_ro:AF019048	+ 1476.50	2140.98	3.9e-111	864	AB032771 Mus musculus RANKL 2 m
gb_ro:AB032771	+ 1417.50	2047.47	6.4e-106	2201	AF019047 Homo sapiens receptor
gb_pt3:AF019047	+ 1417.50	2047.21	6.6e-106	2271	AF053712 Homo sapiens osteop
gb_pt3:AF053712	+ 1283.00	1860.73	1.6e-95	754	AB032772 Mus musculus RANKL 3 m
gb_ro:AB032772	+ 1105.00	1600.16	5.2e-81	930	AB037599 Homo sapiens mRNA for
gb_pt1:AB037599	+ 1101.00	1588.79	2.3e-80	1823	AF013171 Homo sapiens TNF-rela
gb_pt3:AF013171	+ 752.00	1080.41	4.7e-52	2029	AB022039 Mus musculus DNA for
gb_ro:AB022039	- 690.00	957.04	3.5e-45	113451	AC023297 Homo sapiens clone
gb_hlg10:AC023297	+ 690.00	952.15	6.5e-45	205139	ALJ19382 Homo sapiens chrom
gb_hlg18:ALJ19382	+ 388.00	559.17	5.1e-23	764	AB022036 Mus musculus DNA for c
gb_ro:AB022036	+ 286.00	414.89	5.5e-15	468	AB022037 Mus musculus DNA for c
gb_ro:AB022036S2	+ 260.50	371.20	1.5e-12	1042	U57059 Homo sapiens Apo-2 ligu
gb_pt6:HSU07059	+ 260.50	366.92	2.6e-12	1751	AF012156 Sequence 1 from paten
gb_pt6:AR012156	+ 260.50	366.83	2.6e-12	1769	U37518 Human TNF-related apopt
gb_pt6:HSU07518	+ 254.50	360.24	6.1e-12	1366	AF012158 Sequence 5 from paten
gb_pat:AR012158	+ 254.50	360.24	6.1e-12	1366	U37522 Mus musculus TNF-relate
gb_ro:MMU037522	+ 224.00	315.00	2.0e-09	1521	AF012157 Sequence 3 from paten
gb_pat:AR012157	+ 221.50	319.40	1.1e-09	575	AB022038 Mus musculus DNA for c
gb_ro:AB022036S3	- 221.50	273.37	4.2e-07	151941	AC016938 Homo sapiens chrom
gb_hlg6:AC016938	+ 221.50	272.55	4.7e-07	167810	AC007051 Homo sapiens chrom
gb_pt2:AC007051	+ 215.50	262.62	1.7e-06	194030	AC010969 Homo sapiens chrom
gb_hlg3:AC010969	+ 185.50	263.69	1.5e-06	864	U48469 B.taurus mRNA for CD40 l
gb_o:BTCD40LIG	+ 183.00	260.34	2.2e-06	834	E11348 Rat cDNA encoding Fas an
em_pat:E11348	+ 183.00	254.85	4.5e-06	1623	U03470 Rattus norvegicus Fas a
gb_ro:RNU03470	+ 183.00	254.85	4.5e-06	1623	E11353 Rat cDNA encoding Fas a
em_pat:E11353	+ 182.00	258.86	2.7e-06	837	E11349 Mouse cDNA encoding Fas
em_pat:E11349	+ 182.00	258.02	3.0e-06	927	E11355 Mouse cDNA encoding Fas
em_pat:E11355	+ 182.00	253.82	5.1e-06	1541	U10984 Mus musculus C57BL/6 Fa
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DEFINITION Mus musculus mRNA for osteoclast differentiation factor (ODF),
complete cds.
ACCESSION AB008426
VERSION AB008426.1 GI:3041781
KEYWORDS osteoclast differentiation factor (ODF).
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ORGANISM Mus musculus
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Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Yasuda,H., Shima,N., Nakagawa,N., Yamauchi,K., Kinoshita,M.,
Mochizuki,S., Tomoyasu,A., Yano,K., Goto,M., Murakami,A., Tsuda,E.,
Moriyaga,T., Higashio,K., Udagawa,N., Takahashi,N. and Suda,T.
TITLE Submitted (22-OCT-1997) to the DBJ/EMBL/GenBank databases.
JOURNAL Hisataka Yasuda, Snow Brand Milk Products Co., Ltd., Research
Institute of Life Science, 519 Shimo-Ishibashi, Ishibashi-machi,
Tochigi 329-05, Japan (E-mail:fvbd7042emb.infoweb.or.jp,
Tel:0285-52-1331, Fax:0285-53-1314)
2 (sites)

REFERENCE
AUTHORS Yasuda,H., Shima,N., Nakagawa,N., Yamauchi,K., Kinoshita,M.,
Mochizuki,S., Tomoyasu,A., Yano,K., Goto,M., Murakami,A., Tsuda,E.,
Moriyaga,T., Higashio,K., Udagawa,N., Takahashi,N. and Suda,T.
TITLE Submitted (22-OCT-1997) to the DBJ/EMBL/GenBank databases.
JOURNAL Hisataka Yasuda, Snow Brand Milk Products Co., Ltd., Research
Institute of Life Science, 519 Shimo-Ishibashi, Ishibashi-machi,
Tochigi 329-05, Japan (E-mail:fvbd7042emb.infoweb.or.jp,
Tel:0285-52-1331, Fax:0285-53-1314)
2 (sites)

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ACCESSION AB036798

VERSION AB036798.1 GI:8843829

KEYWORDS RANKL 1.

SOURCE Mus musculus cDNA to mRNA.

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 951)
AUTHORS Ikeda,T.
TITLE RANKL 1
JOURNAL Published Only in DataBase (2000) In press
REFERENCE 2 (bases 1 to 951)
AUTHORS Ikeda,T.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-2000) to the DDBJ/EMBL/GenBank databases. Tohru Ikeda, School of Medicine, Tokyo Medical and Dental University, Department of Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8519, Japan (E-mail: toru.pth2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)

FEATURES Location/Qualifiers

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ORIGIN

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Quality: 1675.00 Length: 316

Ratio: 5.301 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

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DEFINITION Mus musculus TNF-related ligand TRANCE mRNA, complete cds.
ACCESSION AF013170
VERSION AF013170.1 GI:2411497
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 2237) Wong,B.R., Rho,J., Arron,J., Robinson,E., Orlinick,J., Chao,M., Kalachikov,S., Cayani,E., Bartlett,P.S. III, Frankel,W.N., Lee,S.Y. and Choi,Y.
TITLE	TRANCE is a novel ligand of the tumor necrosis factor receptor family that activates c-Jun N-terminal kinase in T cells
JOURNAL	J. Biol. Chem. 272 (40), 25190-25194 (1997)
MEDLINE	97460112
REFERENCE	2 (bases 1 to 2237)
AUTHORS	Wong,B.R., Josien,R., Lee,S.Y., Sauter,B., Li,H.L., Steinman,R.M. and Choi,Y.
TITLE	TRANCE (tumor necrosis factor [TNF]-related activation-induced cytokine), a new-TNF family member predominantly expressed in T cells, is a dendritic cell-specific survival factor
JOURNAL	J. Exp. Med. 186 (12), 2075-2080 (1997)
MEDLINE	98060869
REFERENCE	3 (bases 1 to 2237)
AUTHORS	Fuller,K., Wong,B., Fox,S., Choi,Y. and Chambers,T.J.
TITLE	TRANCE is necessary and sufficient for osteoblast-mediated activation of bone resorption in osteoclasts
JOURNAL	J. Exp. Med. 188 (5), 997-1001 (1998)
MEDLINE	98401035
REFERENCE	4 (bases 1 to 2237)
AUTHORS	Wong,B.R., Josien,R., Lee,S.Y., Vologodskaia,M., Steinman,R.M. and Choi,Y.
TITLE	THE TRAF family of signal transducers mediates NF-kappaB activation by the TRANCE receptor
JOURNAL	J. Biol. Chem. 273 (43), 28355-28359 (1998)
MEDLINE	98447691
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AUTHORS	Wong,B.R., Rho,J., Arron,J., Lee,S.Y., Robinson,E. and Choi,Y.
TITLE	Direct Submission
JOURNAL	Submitted (09-JUL-1997) Howard Hughes Medical Institute, The Rockefeller University, 1230 York Ave., New York, NY 10021, USA
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2295)
AUTHORS Boyle,W.J.
TITLE Osteoprotegerin binding proteins
JOURNAL Patent: US 5843678-A 6 01-DEC-1998;
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ACCESSION AF053713
VERSION AF053713.1 GI:3057147
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SOURCE house mouse.
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REFERENCE 1 (bases 1 to 2299)
AUTHORS Lacey,D.L., Fims,E., Tan,H.-L., Kelley,M.J., Dunstan,C.R.,
Burgess,T., Elliott,R., Colombero,A., Elliott,G., Scully,S.,
Hsu,H., Sullivan,J., Hawkins,N., Davy,E., Capparelli,C., Eli,A.,
Qian,Y.-X., Kaufman,S., Sarosi,I., Shalhoub,V., Senaldi,G., Guo,J.,
Delaney,J. and Boyle,W.J.
TITLE Osteoprotegerin ligand is a cytokine that regulates osteoclast
differentiation and activation
JOURNAL Cell 93 (2), 165-176 (1998)
MEDLINE 98227661
REFERENCE 2 (bases 1 to 2299)
AUTHORS Boyle,W.J.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,
One Amgen Center Drive, Thousand Oaks, California 91320, USA
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 DEFINITION (RANKL) mRNA, complete cds
 ACCESSION AF019048
 VERSION AF019048.1 GI:2612923
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 1 (bases 1 to 2225)
 Anderson, D.M., Maraskovsky, E., Billingsley, W.L., Dougall, W.C.,
 Tonetsko, M.E., Roux, E.R., Teepe, M.C., DuBoise, R.F., Cosman, D., and
 Galibert, L.
 TITLE A homologue of the TNF receptor and its ligand enhance T-cell
 growth and dendritic-cell function
 JOURNAL Nature 390 (6656), 175-179 (1997)
 MEDLINE 98032977
 REFERENCE 2 (bases 1 to 2225)
 Anderson, D.M., Billingsley, W., Dougall, W., Maraskovsky, E.,
 Cosman, D., DuBoise, R. and Galibert, L.
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 Ixkeda, T.
 1 (bases 1 to 864)
 Receptor activator of NF-kB ligand 2
 TITLE Published Only in DataBase (2000) In press
 REFERENCE 2 (bases 1 to 864)
 Ixkeda, T.
 Direct Submission
 Submitted (28-SEP-1999) to the DDBJ/EMBL/GenBank databases. Tohru Ixkeda, School of Medicine, Tokyo Medical and Dental University, Department of Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113-8519, Japan (E-mail: toru.iph2@med.tmd.ac.jp, Tel:81-3-5803-5176, Fax:81-3-5803-0123)
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VERSION AF019047.1 GI:2612921
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2201)
AUTHORS Anderson,D.M., Maraskovsky E., Billingsley,W.L., Dougall,W.C.,
Tometsko,M.E., Roux,E.R., Teepe,M.C., DuBoise,R.F., Cosman,D. and
Galibert,L.
TITLE A homologue of the TNF receptor and its ligand enhance T-cell
growth and dendritic-cell function
JOURNAL Nature 390 (6656), 175-179 (1997)
MEDLINE 98032977
REFERENCE 2 (bases 1 to 2201)
AUTHORS Anderson,D.M., Billingsley W., Dougall,W., Maraskovsky,E.,
Cosman,D., DuBoise,R. and Galibert,L.
TITLE Direct Submission
JOURNAL Submitted (13-AUG-1997) Molecular Biology, Immunex Corp., 51
University St., Seattle, WA 98101, USA
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REFERENCE 1 (bases 1 to 2271)
AUTHORS Lacey, D.L., Timms, E., Tan, H.-L., Kelley, M.J., Dunstan, C.R.,
Burgess, T., Elliott, R., Colombero, A., Elliott, G., Scully, S.,
Hsu, H., Sullivan, J., Hawkins, N., Davy, E., Capparelli, C., Eli, A.,
Qian, Y.-X., Kaufman, S., Sarosi, I., Shalhoub, V., Senaldi, G., Guo, J.,
Delaney, J., and Boyle, W.J.
TITLE Osteoprotegerin ligand is a cytokine that regulates osteoclast
differentiation and activation
JOURNAL Cell 93 (2), 165-176 (1998)
MEDLINE 98227661
REFERENCE 2 (bases 1 to 2271)
AUTHORS Boyle, W.J.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-1998) Department of Cell Biology, Amgen, Inc.,
One Amgen Center Drive, Thousand Oaks, California 91320, USA
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complete cds.
ACCESSION AB032772
VERSION AB032772.1 GI:8843824
KEYWORDS receptor activator of NF-kB ligand 3.
SOURCE Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (sites)
Ikeda,T., Takahashi,H. and Hirokawa,K.
Somatostatin, a new marker of osteoblast, regulates the expression
of RANKL isoforms
Unpublished (1999)
2 (bases 1 to 754)
Ikeda,T.
Direct Submission
Submitted (28-SEP-1999) to the DDBJ/EMBL/GenBank databases. Tooru
Ikeda, School of Medicine, Tokyo Medical and Dental University,
Department of Pathology and Immunology; 1-5-45 Yushima, Bunkyo-ku,
Tokyo 113-8519, Japan (E-mail:tooru.pth2@med.tmd.ac.jp,
Tel:81-3-5803-5176, Fax:81-3-5803-0123)
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (sites)
Nagai,M., Kyakumoto,S. and Sato,N.
Cancer cells responsible for humoral hypercalcemia express mRNA
encoding a secreted form of ODF/TRANCE that induces osteoclast
formation
Biochem. Biophys. Res. Commun. 269 (2), 532-536 (2000)

JOURNAL
MEDLINE
20175237
REFERENCE
2 (bases 1 to 930)
Nagai,M., Kyakumoto,S. and Sato,N.
Direct Submission
Submitted (26-JAN-2000) to the DDBJ/EMBL/GenBank databases.
Masazumi Nagai, Iwate Medical University School of Dentistry,
Department of Biochemistry; 19-1 Uchinamaru, Morioka, Iwate 020-8505,
Japan (E-mail:mnagai@iwate-med.ac.jp, Tel:+81-19-651-5111(ex.4436),
Fax:+81-19-654-4147)

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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1823)
AUTHORS Wong,B.R., Rho,J., Arron,J., Robinson,E., Orlinick,J., Chao,M.,
Kalachikov,S., Cayani,E., Bartlett,F.S. III, Frankel,W.N., Lee,S.Y.
and Choi,Y.
TITLE TRANCE is a novel ligand of the tumor necrosis factor receptor
family that activates c-Jun N-terminal kinase in T cells
JOURNAL J. Biol. Chem. 272 (40), 25190-25194 (1997)
MEDLINE 97460112
REFERENCE 2 (bases 1 to 1823)
AUTHORS Wong,B.R., Rho,J., Arron,J., Lee,S.Y., Robinson,E. and Choi,Y.
TITLE Direct Submission
JOURNAL Submitted (09-JUL-1997) Howard Hughes Medical Institute, The
Rockefeller University, 1230 York Ave., New York, NY 10021, USA
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Ratio: 4.705 Gaps: 1
Percent Similarity: 95.510 Percent Identity: 84.082
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US-08-989-362-2 x AF013171 ..
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74 GlnMetAspProAsnArgIleSerGluAspSerThrHisCysPheTyrAr 90
|||||.....:|||||.....:|||||.....:|||||.....:|||||
1 CAGATGCATCCTAATAGAAATATCAGAAGATGGCACTCCTCATTTATAG 50
90 gileLeuArgLeuHisGluAsnAlaGlyLeuGlnAspSerThrLeuGluS 107
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[illegible]

seq_name: qb_ro:AB022036S4

seq_documentation_block:	
LOCUS	AB022036S4
DEFINITION	Mus musculus DNA for osteoclast differentiation factor, exon 5, complete cds.
ACCESSION	AB022039
VERSION	AB022039.1 GI:4127268
KEYWORDS	osteoclast differentiation factor.
SEGMENT	4 of 4
SOURCE	Mus musculus (strain:129) embryonic stem cell DNA.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (sites) Kodaira.K., Kodaira.K., Mizuno.A., Yasuda.H., Shima.N., Murakami.A., Ueda.M. and Higashio.K.
TITLE	Cloning and characterization of the gene encoding mouse osteoclast differentiation factor

293 rAsnProSerLeuLeuAspProAspGlnAspAlaThrTyrPheGlyAlap 310
|||||
508 CACCCCTTCCTGCTGGATCCGATCAAGATGCGACGTACTTTGGGCTT 557
|||||
310 helysValGlnAspIleAsp 316
|||||
558 TCAAAGTTCAGGACATGAC 577
|||||

seq_name: gb_htg10:AC023297

seq_documentation_block:
LOCUS AC023297 113451 bp DNA HTG 03-MAR-2000
DEFINITION Homo sapiens clone RP11-21H9, WORKING DRAFT SEQUENCE, 13 unordered
pieces.
ACCESSION: AC023297
VERSION AC023297.3 GI:7144965
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE
human.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 113451)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-21H9
Unpublished

2 (bases 1 to 113451)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Balgwin,J., Barna,N., Beda,P., Boguslavsky,L.,
Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Choepei,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P.,
Dearellano,K., Dewar,K., Dodge,S., Domino,M., Doyle,M.,
Fenster,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Landers,T., Largocque,K., Lehoczy,J., Levine,R.,
Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N., McCarthy,M.,
McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J.,
Meneus,L., Mithova,T., Miranda,C., Mlenga,V., Morrow,J., Naylor,J.,
Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Olivar,T.M.,
Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C.,
Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S.,
Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A.,
Travers,M., Triggilio,J., Vassiliev,H., Viel,R., Vo.A., Willson,B.,
Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and
Zody,M.

Direct Submission
Submitted (11-FEB-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 3, 2000 this sequence version replaced gi:7139552.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L4020
Center clone name: 21_H_9

----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 106493 bases at least Q40
Consensus quality: 109791 bases at least Q30
Consensus quality: 111178 bases at least Q20
Insert size: 138000; agarose-1p
Insert size: 112251; sum-of-contrigs
Quality coverage: 3.5 in Q20 bases; agarose-1p
Quality coverage: 4.3 in Q20 bases; sum-of-contrigs

TITLE
JOURNAL
COMMENT

* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 2264: contig of 2264 bp in length
* 2265 2364: gap of 100 bp
* 2365 6779: contig of 4415 bp in length
* 6780 6879: gap of 100 bp
* 6880 11332: contig of 4453 bp in length
* 11333 11432: gap of 100 bp
* 11433 17335: contig of 5903 bp in length
* 17336 17435: gap of 100 bp
* 17436 23308: contig of 5873 bp in length
* 23309 23408: gap of 100 bp
* 23409 28598: contig of 5190 bp in length
* 28599 28698: gap of 100 bp
* 28699 36183: contig of 7485 bp in length
* 36184 36283: gap of 100 bp
* 36284 44529: contig of 8246 bp in length
* 44530 44629: gap of 100 bp
* 44630 53672: contig of 9043 bp in length
* 53673 53772: gap of 100 bp
* 53773 62948: contig of 9176 bp in length
* 62949 63048: gap of 100 bp
* 63049 75673: contig of 12625 bp in length
* 75674 75773: gap of 100 bp
* 75774 92375: contig of 16602 bp in length
* 92376 92475: gap of 100 bp
* 92476 113451: contig of 20976 bp in length.

FEATURES
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/db_xref="taxon:9606"
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/clone_lib="RPC1-11 Human Male BAC"
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17436..23308
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23409..28598
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BASE COUNT 34163 a 23042 c 23371 g 1200 others
ORIGIN

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		/db_xref="taxon:9606"	
		/chromosome="13"	
		/clone="RP11-86N24"	
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		1. 19230	
misc_feature		/note="assembly_fragment:00871"	
		clone_end:T7	
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		/note="assembly_fragment:01284"	
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		/note="assembly_fragment:00429"	
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		fragment_chain:3	
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		fragment_chain:5	
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		fragment_chain:6	
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misc_feature      183862. .188214
                  /note="assembly_fragment:01354"
misc_feature      188315. .205139
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clone_end:sp6
vector_side:right"
BASE COUNT      59553 a 41164 c 41807 g 59990 t 2625 others
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    Quality:      690.00      Length:      141
    Ratio:        5.000      Gaps:      0
Percent Similarity: 97.872      Percent Identity: 90.071
alignment_block:
US-08-989-362-2 x ALJ39382 ..
Align seg 1/1 to: ALJ39382 from: 1 to: 205139
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      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
192  pAlaLysIleSerAsnMetThrLeuSerAsnGlyLysLeuArgValAsnG 209
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
135140 GGCCAAGATCTCCAACATGACTTTTAGCAATGGAAACTAATAGTTAATC 135189
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
209  lnAspGlyPheTyrTyrLeuTyrAlaAsnIleCysPheArgHisGlu 225
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
135190 AGGATGGCTTTTATTACTGTATGCCAACATTTCTGTCGCATCATGAA 135239
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
226  ThrSerGlySerValProThrAspTyrLeuGlnLeuMetValTyrValVa 242
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
135240 ACTTCAGGAGACCTAGCTACAGAGATCTTCAACTAATGGTGATCGTCA 135289
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
242  llyThrSerIleLysIleProSerSerHisAsnLeuMetLysGlyGlyS 259
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
135290 TAAACCAGCATCAAAATCCCAAGTTCTCATACCTGTATGAAGAGAGAA 135339
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
259  erThrLysAsnTrpSerGlyAsnSerGluPheHisPheTyrSerIleAsn 275
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
135340 GCACCAAGTATTGGTCAGGGAATTCGAATTCCAATTTTATTTCATAAAC 135389
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276  ValGlyGlyPhePheLysLeuArgAlaGlyGluGluIleSerIleGlnVa 292
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
135390 GTTGGTGGATTTTAAAGTTACGGTCTGGAGAGGAATTCAGCATCGAGT 135439
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
292  lSerAsnProSerLeuLeuAspProAspGlnAspAlaThrTyrPheGlyA 309
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
135440 CTCCAACCCCTCTTACTGGATCCGGATCAGGATGCACATACATTTGGG 135489
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
309  laPheLysValGlnAspIleAsp 316
      ::::::::::::::::::::::::::::::::::::::::::::::::::::::
135490 CTTTTAAAGTTCGAGATATAGAT 135512
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alignment_block:

US-08-989-362-2 x V69900

Align seg 1/1 to: V69900 from: 1 to: 951

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1 ATCGCGCGGCGCAGCGAGACTAGCGCAATACCTGCGCAGCTCGGAGGA 50
|||||
17 uMetGlySerGlyProGlyValProHisG: uGlyProLeuHisProAlap 34
|||||
51 GATGGCGAGCGCGCGCGCTCCACACG/GGGTCCGCTGCACCCCGCGC 100
|||||
34 roSerAlaProAlaProAlaProProProlaAlaSerArgSerMetPhe 50
|||||
101 CTCTCTCACCGCTCGCGCGCGCCACCC CCGCCTCCCGCTCCATGTT 150
|||||
51 LeuAlaLeuLeuGlyLeuGlyLeuGlyGlyValValCysSerIleAlaLe 67
|||||
151 CTGGCCCTCTCTGGGGCTGGGACTGGGCCAC GTGGTCTGCAGCATCGCT 200
|||||
67 uPheLeuTyrPheArgAlaGlnMetAspP: oAsnArgIleSerGluAspS 84
|||||
201 GTTCCTGTACTTTCGAGCGCAGATGGATC TACAGATATACAGAGACA 250
|||||
84 erThrHisCysPheTyrArgIleLeuArgIleuHisGluAsnAlaGlyLeu 100
|||||
251 GCACCTCACTGCTTTTATAGAACTCCTCAGAC TCCATGAAACCGCAGGTTG 300
|||||
101 GlnAspSerThrLeuGluSerGluAspThrLeuProAspSerCysArgAr 117
|||||
301 CAGGACTCGACTCTGGAGAGTGAAGACACACTACCTGACTTCCTGCAGGAG 350
|||||
117 gMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnHisIleV 134
|||||
351 GATGAACACAGCCTTTTCAGGGGCGCTGCAGAAGGAACCTCAACACATTG 400
|||||
134 alGlyProGlnArgPheSerGlyAlaProAlaMetMetGluGlySerTrp 150
|||||
401 TGGGGCCACAGCGCTTCTCAGGAGCTCCAGCTATGATGGAAGCGTCATGG 450
|||||
151 LeuAspValAlaGlnArgGlyLysProGluAlaGlnProPheAlaHisLe 167
|||||
451 TTGGATGTGGCCAGCGAGGCAAGCGCTGAG3CCAGGCCATTTTCACACCT 500
|||||
167 uThrIleAsnAlaAlaSerIleProSerGlySerHisLysValThrLeus 184
|||||
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|||||
184 erSerTrpTyrHisAspArgGlyTrpAlaLysIleSerAsnMetThrLeu 200
|||||
551 CCTCTTGGTACCACGATCGAGGCTGGGCCAAGATCTCTAACATGACGTTA 600
|||||
201 SerAsnGlyLysLeuArgValAsnGlnAsp: yPheTyrTyrLeuTyrAl 217
|||||
601 AGCAACGGAAACTAAGGGTTTACCAAGAT:GCTTCTATTACCTGTACGC 650
|||||
217 aAsnIleCysPheArgHisGluThrSe: GlySerValProThrAspF 234
|||||
651 CAACATTGCTTTCGGCATCATGAACATC:GGAAGCGTACCTTACAGACT 700
|||||
234 yrLeuGlnLeuMetValTyrValValLysTr:SerIleLysIleProSer 250
|||||
701 ATCTTCAGCTGATGGTGTATGCTGTTAAAA: CAGCATCAAAATCCCAAGT 750
|||||
251 SerHisAsnLeuMetLysGlyGlySerThr: yAsnTrpSerGlyAsnSe 267
|||||
751 TCTCATAACCTGATGAAGAGGAGGAGCAG:AAAACCTGGTGGGCAATTC 800
|||||
267 rGluPheHisPheTyrSerIleAsnValGL: GlyPhePheLysLeuArgA 284
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alignment_scores:

Quality: 1675.00

Length: 316

Ratio: 5.301

Gaps: 0

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301 AspGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspIleAsp 316
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901 GATCAAGATGCGAGCTACTTTGGGGCTTTCAAGTTCAGGACATAGAC 948
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AC 299965;
XX
DT 25-JUL-2000 (first entry)
XX
DE DNA encoding a murine osteoprotegerin ligand (OPGL).
XX
KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
KW tumour necrosis factor receptor; type II transmembrane protein;
KW osteoclast differentiation; CSF-1; osteoclast activator;
KW immune response; osteoporosis; bone resorption; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 1..951
FT /tag= a
FT /product= "osteoprotegerin ligand"
XX
PN W0200015807-A1.
XX
PD 23-MAR-2000.
XX
PF 13-SEP-1999; 99WO-DK00481.
XX
PR 15-SEP-1998; 98BK-0001164.
PR 02-OCT-1998; 98US-0102896.
XX
PA (MEBI-) M & E BIOTECH AS.
XX
PI Halkier T, Haanling J;
XX
WP1: 2000-271444/23.
P-PSDB; Y84418.
XX
PT In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
to treat, prevent and ameliorate osteoporosis -
XX
PS Disclosure; Page 79-81; 110pp; English.
XX
CC The present sequence encodes a murine osteoprotegerin ligand (OPGL).
CC Osteoprotegerin is a secreted member of the tumour necrosis factor
CC receptor family, which blocks osteoclastogenesis in a dose dependent
CC manner. The OPGL protein is synthesised as a type II transmembrane
CC protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
CC is a potent osteoclast differentiation factor when combined with CSF-1.
CC It is not capable of inducing osteoclast differentiation in the absence
CC of CSF-1. OPGL is also an activator of mature osteoclasts. The
CC specification describes a method for the in vivo down-regulation of
CC OPGL activity in an animal. The method comprises using at least one OPGL
CC polypeptide or subsequence, and/or at least one OPGL analogue to induce
CC an immune response in the animal. The method and OPGL polypeptide are
CC useful for treating, preventing and ameliorating osteoporosis or other
CC diseases or conditions characterised by excessive bone resorption.
XX
SQ Sequence 951 BP; 231 A; 267 C; 248 G; 205 T; 0 other;
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Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-08-989-362-2 x z99965 ..
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17 uMetGlySerGlyProGlyValProHisGluGlyProLeuHisProAlap 34
51 GATGGGCGCGGCCCGCGCTCCACAGAGGGTCCGCTGCACCCCGCGC 100
34 roSerAlaProAlaProAlaProProProAlaLaSerArgSerMetPhe 50
101 CTTCTGCACCGGCTCCGGCGCGCCACCCGCGCTCCGCTCCCATGTC 150
51 LeuAlaLeuLeuGlyLeuGlyLeuGlyValValValCysSerIleAlaLe 67
151 CTGCCCCCTCTGGGGCTGGGACTGGCGCAGGTGTCTGCACATCGCTCT 200
67 uPheLeuTyrPheArgAlaGlnMetAspProAsnArgIleSerGluAspS 84
201 GTTCCTGTACTTTCGAGCGCATGGATCCTAACAGAAATATCAGAAGA 250
84 erThrHisCysPheTyrArgIleLeuArgLeuHisGluAsnAlaGlyLeu 100
251 GCACCTACTGCTTTATAGATCTCGAGACTCCATGAACACGAGGTTG 300
101 GlnAspSerThrLeuGluSerGluAspThrLeuProAspSerCysArgAr 117
301 CAGGACTCGACTCTGGAGAGTGAAGACACACTAGCTACTCTCTGCAGAG 350
117 gMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnHisIleV 134
351 GATGAACAAAGCCTTTCAGGGGGCGGTGCAAGAGAACTGCAACACATG 400
134 alGlyProGlnArgPheSerGlyAlaProAlaMetMetGluGlySerTrp 150
401 TGGGGCCACAGCGCTTCTCAGGAGCTCCAGCTATGATGAGAGGCTCATG 450
151 LeuAspValAlaGlnArgGlyLysProGluAlaGlnPropheAlaHisLe 167
451 TTGGATGTGGCCACAGCGAGGCAAGCCTCAGGCCCGCCAGCCATTTGCACACCT 500
167 uThrIleAsnAlaAlaSerIleProSerGlySerHisLysValThrLeuS 184
501 CACCATCAATGCTGCCAGCATCCCATCGGGTCCCATAAAGTCACTCTGT 550
184 erSerTrpTyrHisAspArgGlyTrpAlaLysIleSerAsnMetThrLeu 200
551 CCTCTGGTACCAGCATCGAGGCTGGGCCAAGATCTCTAACATGACGTTA 600
201 SerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTyrLeuTyrAl 217
601 AGCAACGGAAAACTAAGGTTAACCAAGATGCTTCTATTACCTCTACGC 650
217 aAsnIleCysPheArgHisHisGluThrSerGlySerValProThrAspTr 234
651 CAACATTTGCTTTCGGCATCATGAACATCGGGAAGCGTACCTACAGACT 700
234 yrLeuGlnLeuMetValTyrValValLysThrSerIleLysIleProSer 250
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251 SerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerGlyAsnSe 267
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267 rGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLysLeuArgA 284

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284 laGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeuAspPro 300
851 CTGGTGAAGAAATTAGCATTCAGTGTCCAAACCTTCCCTCTGGATCCG 900
301 AspGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspIleAsp 316
901 GATCAAGATCGGACGACTTGTGGGCTTTCAAAGTTCCAGGACATAGAC 948
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XX z49024;
XX AC
XX DT
XX 31-MAR-2000 (first entry)
XX DE Osteoclast formation promoting factor coding sequence.
XX KW OBM-BP; OBM binding protein; osteoclast formation promoting factor;
XX KW bone metabolic disease; osteoporosis; therapy; ss.
XX OS Mus sp.
XX JN JP11332581-A.
XX PD 07-DEC-1999.
XX PF 20-OCT-1998; 98JP-0316973.
XX PR 24-MAR-1998; 98JP-0076232.
XX PA (SNOW) SNOW BRAND MILK PROD CO LTD.
XX PA (SANY) SANKYO CO LTD.
XX DR WPI; 2000-091362/08.
XX A new protein, a DNA and its application -
XX Example 1; Page 13; 18pp; Japanese.
XX CC This sequence encodes the osteoclast formation promoting factor (OBM).
CC The invention relates to an OBM binding protein (OBM-BP). The protein is
CC useful as a preventive and/or treating agent for bone metabolic diseases
CC such as osteoporosis. Substances which inhibit the binding of OBM to
CC OBM-BP can be used as biochemical reagents.
XX
SQ Sequence 951 BP; 231 A; 267 C; 248 G; 205 T; 0 other;
alignment_scores:
Quality: 1675.00 Length: 316
Ratio: 5.301 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
alignment_block:
US-08-989-362-2 x z49024 ..
Align seg 1/1 to: z49024 from: 1 to: 951
1 MetArgArgAlaSerArgAspTyrGlyLysTyrLeuArgSerSerGluGl 17
1 ATGCGCGGGCCAGCCGAGACTACGGCAAGTACCCTGCCGACGTCGGAGGA 50
17 uMetGlySerGlyProGlyValProHisGluGlyProLeuHisProAlap 34
51 GATGGGCGCGGCCCGCGCTCCACAGAGGGTCCGCTGCACCCCGCGC 100
34 roSerAlaProAlaProAlaProProProAlaLaSerArgSerMetPhe 50
101 CTTCTGCACCGGCTCCGGCGCGCCACCCGCGCTCCGCTCCCATGTC 150

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51  LeuAlaLeuLeuGlyLeuGlyLeuGlyLeuGlyValValValCysSerIleAlaLe 67
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151 CTGGCCCTCTGGGGTGGGACATGGGCCAAGTGTCTGCGACATCGCTCT 200
|||||
67  uPheLeuTyrPheArgAlaGlnMetAspProAsnArgIleSerGluAspS 84
|||||
201 GTTCCTGTACTTTCGAGCGCAGATGATCTTAACAGAAATATCAGAGACA 250
|||||
84  erThrHisCysPheTyrArgIleLeuArgIleHisGluAsnAlaGlyLeu 100
|||||
251 GCACCTCAGTCTTTATAGAACTCTGAGAC TCCATGAAAACGCGAGTTG 300
|||||
101 GlnAspSerThrLeuGluSerGluAspThrLeuProAspSerCysArgAr 117
|||||
301 CAGGACTCGACTCTGGAGAGTGAAGACAC CTACCTGACTCTCTCGAGGAG 350
|||||
117 gMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnHisIleV 134
|||||
351 GATGAACAAGCCCTTCAGGGGCCGTGCTGAAGGAACCTGCAACACATTG 400
|||||
134 aGlyProGlnArgPheSerGlyAlaProAlaMetMetGluGlySerTrp 150
|||||
401 TGGGGCCACAGCCCTCTCAGGAGCTCCAGCTATGATGGAAGCTCATGG 450
|||||
151 LeuAspValAlaGlnArgGlyLysProGluAlaGlnProPheAlaHisLe 167
|||||
451 TTGGATGTGGCCCGCAGCGAGCAAGCCCTGAGCGCCAGCCATTTGCACACCT 500
|||||
167 uThrIleAsnAlaAlaSerIleProSerGlySerHisLysValThrLeuS 184
|||||
501 CACCATCAATGCTGCCAGCATCCCATCGGGTCCCATATAAAGTCACCTGT 550
|||||
184 erSerTrpTyrHisAspArgGlyTrpAlaLysIleSerAsnMetThrLeu 200
|||||
551 CCTCTTGGTACCAGATCGNGGCTGGGCCAGATCTCTACATGACGTTA 600
|||||
201 SerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTyrLeuTyrAl 217
|||||
601 AGCAACGGAAACATAAGGGTTAACCAAGATGCTTCTATTACCTGTACGC 650
|||||
217 aAsnIleCysPheArgHisGluThrSerGlySerValProThrAspT 234
|||||
651 CAACATTTGCTTTCGGCATCATGAACATCAGGAAGCGTACCTACAGACT 700
|||||
234 yrLeuGlnLeuMetValTyrValLysTrpSerIleLysIleProSer 250
|||||
701 ATCTTCAGCTGATGGTGTATGCTGTTAAACACAGCATCAAAATCCCAAGT 750
|||||
251 SerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerGlyAsnSe 267
|||||
751 TCTCATAACTGATGAAGAGGAGGAGCACGAAAACTGGTGGGCAATTC 800
|||||
267 rGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLysLeuArgA 284
|||||
801 TGAATTCCTCACTTATATCCATAAATGTTGGTGGATTTTCAAGCTCCGAG 850
|||||
284 laGlyGluGluIleSerIleGlnValSerAimProSerLeuLeuAspPro 300
|||||
851 CTGGTGAAGAAATATGATTCAGGTGTCCATCCCTCCCTGCTGGATCCG 900
|||||
301 AspGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspIleAsp 316
|||||
901 GATCAAGATGCGACGTACTTTGGGGCTTCTAAGTTCCAGGACATAGAC 948
|||||

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seq_name: /cgn_2/9cndata/geneseq/genes/qn/NA1998.DAT:V69886

seq_documentation_block:

ID V69886 standard; cDNA to mRNA; 1531 BP.

XX
AC
XX

DT 10-FEB-1999 (first entry)

```

XX Nucleic acid encoding an OCIF-binding molecule (OBM).
DE
XX Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
KW osteoclast; bone absorption factor; bone disorder; calcium metabolism;
XX ss.
XX Unidentified.
OS
XX Key Location/Qualifiers
FT CDS 125..1075
/*tag= a
XX
PN W09846644-A1.
XX
XX 22-OCT-1998.
XX
XX 15-APR-1998; 98WO-JP01728.
XX
XX 02-DEC-1997; 97JP-0332241.
PR 15-APR-1997; 97JP-0097808.
PR 09-JUN-1997; 97JP-0151434.
PR 12-AUG-1997; 97JP-0217897.
PR 21-AUG-1997; 97JP-0224803.
XX
XX (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX
XX Goto M, Higashio K, Kinoshita M, Kobayashi F, Morinaga T;
PI Nakagawa N, Shima N, Takahashi K, Tomoyasu A, Tsuda E;
PI Washida N, Yamaguchi K, Yano K, Yasuda H;
XX
XX WPI; 1998-594563/50.
XX
XX Protein binding to osteoclastogenesis inhibitory factor - useful
for, e.g. treatment and investigation of disorders of bone and
calcium metabolism
XX
XX Claim 9; Pages 108-109; 151pp; Japanese.
XX
XX The present sequence encodes an osteoclastogenesis inhibitory factor
(OCIF)-binding molecule (OBM). The protein promotes and supports the
separation and maturation of osteoclasts in the presence of bone
absorption factors such as calcitriol or parathyroid hormone (PTH).
OBM is isolated from stroma cells cultured in the presence of a bone
absorption factor by separation and solubilisation of membrane proteins
then affinity chromatography using OCIF. It exists in a full-sequence
form and a solubilised form (SOBM) which is a shorter chain. OBM may be
used for screening potential inhibitors and modifiers of its biological
activity, and screening for receptors to OBM which mediate its function.
These substances can then be used in the treatment of disorders of bone
function and calcium metabolism. The antibodies can be used for assay
of the protein, for investigative and diagnostic purposes, and as
components of drugs.
XX
SQ Sequence 1538 BP; 382 A; 381 C; 416 G; 359 T; 0 other;

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alignment_scores:

Quality: 1675.00 Length: 316
Ratio: 5.301 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-08-989-362-2 x V69886

Align seg 1/1 to: V69886 from: 1 to: 1538

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17 uMetGlySerGlyProGlyValProHisGluGlyProLeuHisProAlap 34
|||||

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175 GATGGGAGCGGCCCGCGCTCCACACGAGGGTCCGCTGCACCCCGCGC 224
34 roSerAlaProAlaProAlaProProAlaAlaSerArgSerMetPhe 50
|||||
225 CTTCTGACCGGCTCCGCGCGCCACCCGCGCTCCCGCTCCATGTTTC 274
51 LeuAlaLeuLeuGlyLeuGlyLeuGlyGlnValValCysSerIleAlaLe 67
|||||
275 CTGGCCCTCTGGGCTGGGCTGGGCTGGGCTGGTGTCTGCAGCATCGCTCT 324
67 uPheLeuTyrPheArgAlaGlnMetAspProAsnArgIleSerGluAsps 84
|||||
325 GTTCCTGTACTTTCGAGCGCAGATGGATCCTAACAGAATATCAGAAGACA 374
84 erThrHisCysPheTyrArgIleLeuArgLeuHisGluAsnAlaGlyLeu 100
|||||
375 GCACCTCACTCTCTTTATAGAACTCTGAGACTCCATGAAGCGCAGGTTTG 424
101 GlnAspSerThrLeuGluSerGluAspThrLeuProAspSerCysArgAr 117
|||||
425 CAGACCTCGACTCTGGAGAGTGAAGACACACTACCTGACTCCTCGCAGAG 474
117 gMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnHisIleV 134
|||||
475 GATGAACACAGCCCTTTCAGGGGGCGCTGCAGAGGAAGCTGCAACACATG 524
134 aGlyProGlnArgPheSerGlyAlaProAlaMetMetGluGlySerTrp 150
|||||
525 TGGGGCCACAGCGCTTCTCAGGAGCTCCAGCTATGATGAAGGCTCATGG 574
151 LeuAspValAlaGlnArgGlyLysProGluAlaGlnProPheAlaHisLe 167
|||||
575 TTGGATGTGGCCAGCGAGGCAAGCCCTGAGGCCAGCCATTTGCACACCT 624
167 uThrIleAsnAlaAlaSerIleProSerGlySerHisLysValThrLeuS 184
|||||
625 CACCATCAATGCTGCCAGATCCCATCCGGTTCCTCAATAAGTCACTCTGT 674
184 erSerTrpTyrHisAspArgGlyTrpAlaLysIleSerAsnMetThrLeu 200
|||||
675 CCCTCTGGTACCACGATCGAGGCTGGGCCCAAGATCTCTAATACATGACG 724
201 SerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTyrLeuTyrAl 217
|||||
725 AGCAACGGAAACCTAAGGGTTAACCAAGATGGCTCTATTACCTGTACGC 774
217 aAsnIleCysPheArgHisHisGluThrSerGlySerValProThrAspT 234
|||||
775 CAACATTTGCTTTCGGCATCATGAACATCGGGAAGCGTACCTACAGACT 824
234 YrLeuGlnLeuMetValTyrValValLysThrSerIleLysIleProSer 250
|||||
825 ATCTTCAGCTGATGGTGTATGCTGTTAAACACGACATCAAAATCCCAAGT 874
251 SerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerGlyAnse 267
|||||
875 TCTCATAACTGATGAAGAGGAGGAGCACGAAACAACTGGTCGGCCAATTC 924
267 rGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLysLeuArgA 284
|||||
925 TGAATTCACACTTTATTCCTCAATAATGTGGGGATTTTTCNAAGCTCGGAG 974
284 laGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeuAspPro 300
|||||
975 CTGGTGAAGAAATTAGCATTCAGGTGTCCAAACCTCTCCCTGCTGGATCCG 1024
301 AspGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspIleAsp 316
|||||
1025 GATCAAGATCGGACGTACTTCTGGGGCTTTCAAAGTTCAGGACATAGAC 1072
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seq_name: /cgn_2/gcgdata/geneseq/geneseq/NA1998.DAT:V41489

seq_documentation_block:

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ID V41489 standard; cDNA; 2191 BP.
XX
AC V41489;
XX
DT 24-SEP-1998 (first entry)
XX
DE Nucleotide sequence of mouse 499E9 gene.
XX
KW Mouse 499E9 protein; polarised Th1 T cell; immune cell; apoptosis;
KW antagonist; autoimmune disorder; rheumatoid arthritis;
KW systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis;
KW acute inflammatory response; antibody; antigen; cancer; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 125..1072
FT /tag= a
FT /product= "mouse 499E9 protein"
XX
PN WO9825958-A2.
XX
PD 18-JUN-1998.
XX
PE 12-DEC-1997; 97WO-US22766.
XX
PR 13-DEC-1996; 96US-0032846.
XX
PA (SCHE ) SCHERING CORP.
XX
PI Gorman DM, Mattson JD;
XX
DR WPI; 1998-348452/30.
DR P-PSDB; W59654.
XX
PT Mouse cell surface antigen, 499E9 protein - used to treat conditions
PT associated with abnormal physiology or development
XX
PS Claim 4; Pages 8-11; 59pp; English.
XX
CC This is the nucleotide sequence encoding the mouse 499E9 protein, used
CC in the method of the invention to treat conditions associated with
CC abnormal physiology or development. The 499E9 protein is expressed
CC highly on polarised Th1 T cells, binding of 499E9 to its receptor may
CC result in either immune cell expansion or apoptosis. Antagonists of
CC 499E9 may be used to modulate immune responses in abnormal situations,
CC e.g. autoimmune disorders including rheumatoid arthritis, systemic
CC lupus erythematosus, Hashimoto's autoimmune thyroiditis, as well as
CC acute inflammatory responses in which T-cell expansion, activation or
CC immunological T-cell memory play an important role. The antibodies
CC can be used to raise anti-idiotypic antibodies which will be useful
CC in detecting or diagnosing various immunological conditions related to
CC the expression of antigens of 499E9. The antibodies, and fragments of
CC 499E9 can be used in the treatment of conditions associated with
CC abnormal physiology or development, including abnormal proliferation
CC (e.g. cancerous conditions) or degenerative conditions.
XX
SQ Sequence 2191 BP; 605 A; 461 C; 518 G; 607 T; 0 other;
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alignment_scores:

Quality:	1675.00	Length:	316
Ratio:	5.301	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	100.000

alignment_block:

US-08-989-362-2 x V41489 ..

Align seg 1/1 to: V41489 from: 1 to: 2191

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125 ATGCGCCGGCGCCGCGAGACTACGGCAAGTACCTGCGCAGCTCGGAGGA 174
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17 uMetGlySerGlyProGlyValProHisG: uGlyProLeuHisProAlap 34
175 GATGGGAGCGGCGCGCGTCCACAGGAGGGTCCGCTGCACCGCGC 224
34 roSerAlaProAlaProAlaProProAlaAlaSerArgSerMetPhe 50
225 CTTCCTGACCGGCTCGGCGCGCGCCACCGC(CCGGCTCCGCTCATGTTC 274
51 LeuAlaLeuLeuGlyLeuGlyLeuGlyGlyValValCysSerIleAlaLe 67
275 CTGGCCCTCTCTGGGCTGGGACTGGGCA(GTGGTCTGCAGCATCGCTCT 324
67 uPheLeuTyrPheArgAlaGlnMetAspPheAsnArgIleSerGluAspS 84
325 GTTCCTGTACTTCGAGCGCAGATGGATCTTAACAGAAATATCAGAGACA 374
84 erThrHisCysPheTyrArgIleLeuArgIleuHisGluAsnAlaGlyLeu 100
375 GCACCTCACTGCTTTTATAGAACTCCTGAGATCCATGAAGACGAGGTTG 424
101 GlnAspSerThrLeuGluSerGluAspThuLeuProAspSerCysArgAr 117
425 CAGGACTCGACTCTGGAGAGTGAAGACACTCTACCTGACTCTCTGCAGGAG 474
117 gMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnHisIleV 134
475 GATGAACAAGCCCTTTTCAGGGGCGCTGGCfGAAGGAACGTCAACACATTG 524
134 aGlyProGlnArgPheSerGlyValaProfIaMetMetGluGlySerTrp 150
525 TGGGGCCACAGCCCTCTCAGGAGCTCCACCTATGATGAAGGCTCATGG 574
151 LeuAspValAlaGlnArgGlyLysProGluAlaGlnProPheAlaHisLe 167
575 TTGGATGTGCCCGCAGCGAGCAGCTGAGCGCCACGCCATTTGCACACCT 624
167 uThrIleAsnAlaAlaSerIleProSerGlySerHisLysValThrLeuS 184
625 CACCATCAATGCTGCCAGCATCCCATCGGCTGCCATAAAGTCACCTGT 674
184 erSerTrpTyrHisAspArgGlyTTrpAlaIlyIleSerAsnMetThrLeu 200
675 CCTCTGGTACCCAGCATCGAGGCTGGGCCAAGATCTCTAACATGAGCTTA 724
201 SerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTyrLeuTyrAl 217
725 AGCAACGGAAACTAAGGGTTAACCAAGATCGCTTCTATTACCTGTACGC 774
217 aAsnIleCysPheArgHisHisGluThrSerGlySerValProThrAsp 234
775 CAACATTTGCTTTCCGGCATCATGAACATC3GGAAGCGTACCTACAGACT 824
234 yLeuGlnLeuMetValTyrValValLysThrSerIleLysIleProSer 250
825 ATCTTCAGCTGATGGTGTATGCTGCTTAAACACAGCATCAAAATCCCAAGT 874
251 SerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerGlyAsnSe 267
875 TCTCATTAACCTGATGAAGAGGAGGAGCAGCAGAACTGGTGGGGCAATTC 924
267 rGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLysLeuArgA 284
925 TGAATTCACCTTTTATTCATAAATGTTGGGGGATTTTCAAGCTCCGAG 974
284 IaGlyGluGluIleSerIleGlnValSerAInProSerLeuLeuAspPro 300
975 CTGGTGAAGAAATTAGCATTTAGGTGTCCACCCCTCCCTGCTGGATCCG 1024
301 AspGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspIleAsp 316
1025 GATCAAGATCGGACGACTTTTGGGGCTTTTC.AAGTTTCAGGACATAGAC 1072

seq_name: /cqn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:X80224

seq_documentation_block:

ID X80224 standard; cDNA; 2237 BP.

XX X80224;

AC AC

XX 17-AUG-1999 (first entry)

DT Murine TRANCE encoding cDNA.

XX Murine TRANCE encoding cDNA.

DE TRANCE; tumour necrosis factor superfamily; signal transduction; TNF;

KW TNF-related activation induced cytokine; immune response; cancer;

KW autoimmune disease; HIV; hypersensitivity; allergen; ds.

XX Mus musculus.

OS Mus musculus.

XX Key

Location/Qualifiers

142..1092

CDS /*tag= a

XX WO929865-A2.

PN 17-JUN-1999.

XX 14-DEC-1998; 98WO-US26486.

XX 11-DEC-1998; 98US-0989479.

XX 12-DEC-1997; 97US-0989479.

XX 03-MAR-1998; 98US-0034099.

XX (UYRQ) UNIV ROCKEFELLER.

XX Choi Y, Josien R, Steinman R, Won B;

XX WPI; 1999-385609/32.

XX P-PSDB; Y17874.

XX TNF like proteins for treating autoimmunity and cancer

XX Claim 4; Fig 3; 164pp; English.

XX The present sequence encodes murine TNF-related activation induced

XX cytokines (TRANCE). Human or murine TRANCE polypeptides or their

XX variants, fragments, derivatives or analogues may be used as modulators

XX of immune response in a mammal comprising antisense sequences to

XX TRANCE and fusion proteins comprising human and/or murine TRANCE.

XX Agonists and antagonists of TRANCE, can be used to modulate immune

XX response by increasing or decreasing the life span of mature dendritic

XX cells and increasing or decreasing T cell activation. These techniques

XX are especially useful for treating immune system related conditions such

XX as HIV, cancer, autoimmune disease or hypersensitivity to an allergen.

XX The TRANCE polypeptides can be used to increase the viability of

XX dendritic cells in vivo or in vitro, especially when used in conjunction

XX with proteins of the tumour necrosis factor (TNF) superfamily (especially

XX CD40L or TNF-alpha).

XX Sequence 2237 BP; 636 A; 470 C; 519 G; 612 T; 0 other;

alignment_scores:

Quality: 1675.00

Ratio: 5.301

Percent Similarity: 100.000

Percent Identity: 100.000

alignment_block:

US-08-989-362-2 x X80224

Align seg 1/1 to: X80224 from: 1 to: 2237

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142 ATGGCGCGGCGCGGAGAGTACCGCAAGTACCTGCGCAGCTCGGAAGA 191

17 uMetGlySerGlyProGlyValProHisGluGlyProLeuHisProAlap 34
|||||
192 GATGGGCGAGCGGCCCGGCTCCACACGAGAGGTCCGTCACCCCGCGC 241
34 roSerAlaProAlaProAlaProProProAlaLaSerArgSerMetPhe 50
|||||
242 CTTCGACCGCTCCGGCGCGCCACCGCGCTCCGCTCCATGTTTC 291
51 LeuAlaLeuLeuGlyLeuGlyLeuGlyGlnValValCysSerIleAlaLe 67
|||||
292 CTGGCCCTCTGGGGCTGGGACTGGGCCAGGTGCTGTCAGCATCGCTCT 341
67 uPheLeuTyrPheArgAlaGlnMetAspProAsnArgIleSerGluAsp 84
|||||
342 GTTCCTGTACTTCGAGCGCAGATGGATCCTAACAGAAATATCAGAGACA 391
84 erThrHisCysPheTyrArgIleLeuArgLeuHisGluAsnAlaGlyLeu 100
|||||
392 GCACCTCACTGCTTTTATAGAACTCCTGAGACTCCATGAACCGCAGTTTG 441
101 GlnAspSerThrLeuGluSerGluAspThrLeuProAspSerCysArgAr 117
|||||
442 CAGGACTCGACTCTGGAGACTGAAGACACACTACCTGACTCCTTCAGGAG 491
117 gMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnHisIleV 134
|||||
492 GATGAACAACAGCCCTTTCAGGGGGCGGTGCAGAGGAATCTGCAACACAT 541
134 aGlyProGlnArgPheSerGlyAlaProAlaMetMetGluGlySerTrp 150
|||||
542 TGGGGCCACAGCCCTTCTCAGGAGCTCCAGCTATGATGGAAGGCTCATGG 591
151 LeuAspValAlaGlnArgGlyLysProGluAlaGlnProPheAlaHisLe 167
|||||
592 TTGGATGTGCCCGCAGCGAGCCAGCCGTAGCGCCAGCCATTTCACACCT 641
167 uThrIleAsnAlaAlaSerIleProSerGlySerHisLysValThrLeus 184
|||||
642 CACCATCAATGCTGCCAGCATCCCATCGGTTGCCATAAAGTCACTCTGT 691
184 erSerTrpTyrHisAspArgGlyTrpAlaLysIleSerAsnMetThrLeu 200
|||||
692 CCTCTGGTACCAAGCATCGAGGTGGGCCAAGATCTCTAACATGACGTTA 741
201 SerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTyrLeuTyrAl 217
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742 AGCAACGGAAAACTAAGGTTTAAACAGATGGCTTCTATTACCTGTACGC 791
217 aAsnIleCysPheArgHisGluThrSerGlySerValProThrAspTr 234
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792 CAACATTGCTTTCGGCATCATGAACATCGGAAGCGTACCTACAGACT 841
234 yrLeuGlnLeuMetValTyrValLysThrSerIleLysIleProSer 250
|||||
842 ATCTTCAGCTGATGGTGTATGCTGTTAAAAACACGATCAAAATCCCAAGT 891
251 SerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerGlyAsnSe 267
|||||
892 TCTCATAACTGATGAAGAGGAGGACCAAAACCTGGTGGGCAATTC 941
267 rGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLysLeuArgA 284
|||||
942 TGAATTCACACTTTTATTCATAATGTTGGGGATTTTCAAGCTCCGAG 991
284 laGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeuAspPro 300
|||||
992 CTGGTCAAGAAATTAGCATTCAGGTGTCACCAACCTTCCCTGCTGGATCCG 1041
301 AspGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspIleAsp 316
|||||
1042 GATCAAGATCGCAGCTACTTTGGGGCTTTCAAAGTTTCAGGACATAGAC 1089

seq_name: /cgn2_2/gcgdata/geneseq/geneseq/NA1998.DAT:v70284

seq_documentation_block:

ID V70284 standard; DNA; 2295 BP.

XX

AC V70284;

XX

DT 11-FEB-1999 (first entry)

XX

Human osteoprotegerin binding protein encoding DNA from the 32D-F3 ins.
XX
Human; osteoprotegerin binding protein; OPG binding protein; arthritis;
osteoporosis; osteoclast maturation; bone disease; metastasis; ODAR;
hypercalcaemia; osteoclast differentiation and activation receptor;
Paget's disease; ss.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT CDS 158..1108

FT /*tag= a

FT /product= "osteoprotegerin binding protein"

XX

PN WO9846751-A1.

XX

PD 22-OCT-1998.

XX

PF 15-APR-1998; 98WO-US07584.

XX

PR 30-MAR-1998; 98US-0052521.

PR

PR 16-APR-1997; 97US-0842842.

PR

PR 23-JUN-1997; 97US-0880855.

XX

PA (AMGE-) AMGEN INC.

XX

PI Boyle WJ;

XX

XX WPI; 1998-594578/50.

DR

DR P-PSDB; W83194.

XX

Nucleic acid encoding osteoprotegerin binding protein - useful for,
e.g. treating bone diseases by modulating osteoclast differentiation
and for diagnosis

XX

PS Claim 1; Fig 1; 47pp; English.

XX

The present sequence encodes human osteoprotegerin (OPG) binding protein.
Host cells transfected with vectors containing nucleic acid molecules
encoding OPG binding protein are used to produce recombinant OPG binding
protein. OPG binding protein is used in binding assays to determine
osteoprotegerin (OG) in biological samples; to screen for specific
binding agents (particularly agonists and antagonists, including
intracellular proteins); to raise Ab (useful in immunoassays for
detection of OPG binding protein) and to identify compounds that
modulate binding of OPG binding protein to osteoclast differentiation
and activation receptor (ODAR). The nucleic acid molecule encoding OPG
binding protein can be used to detect OPG binding protein-encoding
sequences, e.g. screening for related sequences, also to produce
transgenic animal models, while complementary sequences are used for
antisense regulation of OPG binding protein expression. Modulators of
OPG binding protein, particularly soluble forms of OPG binding protein
or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
disease, periodontal disease, osteoporosis, loosening of prostheses,
optionally in combination with agents that promote bone growth.

XX Sequence 2295 BP; 648 A; 487 C; 538 G; 622 T; 0 other;

SQ

alignment_scores:

Quality: 1675.00 Length: 316

Ratio: 5.301 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-08-989-362-2 x v70284
Align seg 1/1 to: v70284 from: 1 to: 2295
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158 ATGCGCGCGCGCCAGCGAGACTACGGCAA(TACCTGCGCAGCTCGGAGGA 207
17 uMetGlySerGlyProGlyValProHisGlyGlyProLeuHisProAlaP 34
208 GATGGGACGGCGCGCGGTCCACACG/GGGTCGCTGCACCCGCGC 257
34 roSerAlaProAlaProAlaProProProIaAlaSerArgSerMetPhe 50
258 CTTCTGCACCGGCTCGGGCGCGCCACCC/CGCCTCCCGCTCCATGTT 307
51 LeuAlaLeuLeuGlyLeuGlyLeuGlyGly: ValValCysSerIleAlaLe 67
308 CTGGCCCTCTGGGGCTGGGACTGGGCCA GTGGTCTGCAGCATCGCTCT 357
67 uPheLeuTyrPheArgAlaGlnMetAsp; oAsnArgIleSerGluAsps 84
358 GTTCCTGTACTTTCGAGCGCAGATGGATCTTAACAGAAATATCAGAGACA 407
84 erThrHisCysPheTyrArgIleLeuArgIeuHisGluAsnAlaGlyLeu 100
408 GCACCTACCTGCTTTATAGATCTCTGAG/ TCCATGAACGCGAGTTG 457
101 GlnAspSerThrLeuGluSerGluAspThr LeuProAspSerCysArgAr 117
458 CAGGACTCGACTCTGGAGAGTGAAGACAC/ CTACCTGACTCTCTGCAGGAG 507
117 gMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnHisIleV 134
508 GATGAACAAAGCCTTTCAGGGGCGCTGCG/ GAAGGAACCTGCAACATTG 557
134 aGlyProGlnArgPheSerGlyAlaPro/ laMetMetGluGlySerTrp 150
558 TGGGGCCACAGCGCTTCTCAGGAGCTCCA/ CTATGATGGAAGGCTCATGG 607
151 LeuAspValAlaGlnArgGlyLysProGlyAlaGlnProPheAlaHisLe 167
608 TTGGATGTGGCCAGCGAGCGAGCCCTGA/ GCCAGCCATTTGCACACCT 657
167 uThrIleAsnAlaAaSerIleProSerGlySerHisLysValThrLeus 184
658 CACCATCAATGTGCCAGCATCCCATCGG/ TCCCATAAAGTCACCTCTGT 707
184 erSerTrpTyrHisAspArgGlyTrpAlaI lysIleSerAsnMetThrLeu 200
708 CCTCTTGGTACCACGATCGAGGCTGGGCG/ AGATCTCTAACATGACGTTA 757
201 SerAsnGlyLysLeuArgValAlaAsnGlnAsrGlyPheTyrTrpLeuTyrAl 217
758 AGCAACGGAATACTAGGGTTAACCAAGAI/ GGCTTCTATTACCTGTACGC 807
217 aAsnIleCysPheArgHisHisGluThrSerGlySerValProThrAspt 234
808 CAACATTTGCTTTCGGCATCATGAACAT/ CGGAAACGCTACCTACAGACT 857
234 yLeuGlnLeuMetValTyrValValLysfHisSerIleLysIleProSer 250
858 ATCTTCAGCTGATGGTGTATGCTGTTAA/ AACCCAGCATCAAAATCCCAAGT 907
251 SerHisAspLeuMetLysGlyGlySerThr LysAsnTrpSerGlyAsnSe 267
908 TCTCATAACTGATGAAGAGGGAGCAGCA/ AAAAACTGGTCGGCAATTC 957
267 rGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLysLeuArgA 284
958 TGAATTCACCTTTTATTCCATAAATGTT/ GGGGATTTTCAAGCTCCGAG 1007

284 laGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeuAspPro 300
1008 CTGGTGAAGAAATTAGCATTAGGTGTCCAAACCTTCCTCTGGATCCG 1057
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seq_documentation_block:
ID Z99966 standard; DNA; 2299 Bp.
XX Z99966;
XX AC
XX DT 25-JUL-2000 (first entry)
XX DE DNA encoding a murine osteoprotegerin ligand (OPGL).
XX KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
KW tumour necrosis factor receptor; type II transmembrane protein;
KW osteoclast differentiation; CSF-1; osteoclast activator;
KW immune response; osteoporosis; bone resorption; ss.
XX OS Mus musculus.
XX FH Key Location/Qualifiers
FT CDS 170..1120
FT /*tag= a
FT /product= "osteoprotegerin ligand"
XX PN WO200015807-A1.
XX PD 23-MAR-2000.
XX PF 13-SEP-1999; 99WO-DK00481.
XX PR 15-SEP-1998; 98DK-0001164.
XX PR 02-OCT-1998; 98US-0102896.
XX PA (MEBI-) M & E BIOTECH AS.
XX PI Halkier T, Haaning J;
XX WPI: 2000-271444/23.
XX P-PSDB: Y84419.
XX PT In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used
XX to treat, prevent and ameliorate osteoporosis -
XX PS Disclosure: Page 82-85; 110pp; English.
XX CC The present sequence encodes a murine osteoprotegerin ligand (OPGL).
XX Osteoprotegerin is a secreted member of the tumour necrosis factor
XX receptor family, which blocks osteoclastogenesis in a dose dependent
XX manner. The OPGL protein is synthesised as a type II transmembrane
XX protein. The murine and human OPGL polypeptides are 87% homologous. OPGL
XX is a potent osteoclast differentiation factor when combined with CSF-1.
XX It is not capable of inducing osteoclast differentiation in the absence
XX of CSF-1. OPGL is also an activator of mature osteoclasts. The
XX specification describes a method for the in vivo down-regulation of
XX OPGL activity in an animal. The method comprises using at least one OPGL
XX polypeptide or subsequence, and/or at least one OPGL analogue to induce
XX an immune response in the animal. The method and OPGL polypeptide are
XX useful for treating, preventing and ameliorating osteoporosis or other
XX diseases or conditions characterised by excessive bone resorption.
XX SQ Sequence 2299 BP; 641 A; 494 C; 541 G; 623 T; 0 other;

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Ratio: 5.301 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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320 CTGGCCCTCTGGGGCTGGGACTGGCGAGTGGCTGTCGACGATCGCTCT 369
67 uPheLeuTyrPheArgAlaGlnMetAspProAsnArgIleSerGluAspS 84
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117 gMetLysGlnAlaPheGlnGlnGlnValGlnLysGluLeuGlnHisIleV 134
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620 TTGGATGTGCCCCCAGCAGGACGCTGAGCCCGCCAGCCATTTCACACCT 669
167 uThrIleAsnAlaAlaSerIleProSerGlySerHisLysValThrLeuS 184
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1070 GATCAAGATGCGACGCTACTTTGGGCTTTCAAGTTTCAGACATAGAC 1117
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seq_documentation_block:
ID V41377 standard; cDNA; 1630 BP.
XX V41377;
XX
DT 08-OCT-1998 (first entry)
XX
DE NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
XX
KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
KW immune response; inflammatory response; toxic shock; sepsis;
KW RANKL; RANK ligand; tumour necrosis factor; TNF; mouse; ss.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 3..887
FT /*tag= a /product= "murine RANKL (ligand for RANK)"
XX
XX WO9828426-A2.
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XX 02-JUL-1998.
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XX 22-DEC-1997; 97WO-US23775.
XX
XX 14-OCT-1997; 97US-0064671.
PR 23-DEC-1996; 96US-0059978.
PR 07-MAR-1997; 97US-0813509.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Anderson DM, Galibert LJ, Maraskovsky E;
XX
XX WPI; 1998-377657/32.
DR P-PSDB; W69956.
XX
XX New isolated ligand for receptor activator of NF-kappa B - used to
PT develop products for augmenting an immune response for inhibiting an
PT inflammatory response and for protection of cells
XX
XX Claim 25; Pages 55-57; 80pp; English.
XX
XX This cDNA encodes a murine RANKL, a ligand for the RANK (receptor
CC activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a
CC member of the tumour necrosis factor (TNF) family. A soluble RANK
CC may be used for inhibiting activation of NF-kB, by contacting a cell
CC expressing membrane-associated RANK with a soluble RANK which binds to
CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
CC used to induce maturation of dendritic cells and enhance their
CC allo-stimulatory capacity, thereby augmenting an immune response. The
CC soluble RANK polypeptide composition may also be used for regulating an
CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
CC may be useful in ameliorating negative effects of an inflammatory
CC response that result from triggering of RANK, e.g. in treating toxic
CC shock or sepsis, graft-versus-host reactions, or acute inflammatory
CC reactions. They can also be used in adjunct therapy for disease
CC characterised by neoplastic cells that express RANK. RANKL polypeptides
CC can also be used to identify inhibitors of RANK and thus inhibitors of
CC an inflammatory response, and also for protecting RANK-expressing cells

CC from the negative effects of chemotherapy or the presence of high levels
 CC of TNF-alpha. The products can also be used for detection and drug
 CC screening.

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 SQ Sequence 1630 BP; 436 A; 355 C; 319 G; 460 T; 0 other;

alignment_scores:
 Quality: 1554.00 Length: 294
 Ratio: 5.304 Gaps: 0
 Percent Similarity: 99.660 Percent Identity: 99.660

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US-08-989-362-2 x V41377 ..

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seq_documentation_block:

ID V41371 standard; cDNA; 1630 BP.

XX V41371;

XX AC

DT 08-OCT-1998 (first entry)

XX NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.

XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;

KW immune response; inflammatory response; toxic shock; sepsis;

KW RANKL; RANK ligand; tumour necrosis factor; TNF; mouse; ss.

XX Mus musculus.

XX Key Location/Qualifiers

FT CDS 3..887

FT /*tag= a

FT /product= "murine RANKL (ligand for RANK)"

XX PN W09828424-A2.

XX PD 02-JUL-1998.

XX PF 22-DEC-1997; 97WO-US23866.

XX PR 14-OCT-1997; 97US-0064671.

XX PR 23-DEC-1996; 96US-0059978.

XX PR 07-MAR-1997; 97US-0813509.

XX (IMMV) IMMUNEX CORP.

XX Anderson DM, Galibert LJ, Maraskovsky E;

XX WPI; 1998-377655/32.

XX DR P-PSDB; W68292.

XX New isolated receptor activator of necrosis factor-kappa B - useful
 for, e.g. developing products for regulating an immune or
 inflammatory response, treating toxic shock or sepsis

XX Example 7; Pages 55-57; 80pp; English.

XX This cDNA encodes a murine RANKL, a ligand for the RANK (receptor
 CC activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a
 CC member of the tumour necrosis factor (TNF) family. Host cells transformed
 CC or transfected with an expression vector comprising the RANK encoding
 CC nucleic acid can be used to produce recombinant RANK protein. The soluble
 CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to
 CC RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
 CC used for regulating an immune or inflammatory response. Inhibition of
 CC NF-kB by RANK antagonists may be useful in ameliorating negative effects
 CC of an inflammatory response that result from triggering of RANK, e.g. in
 CC treating toxic shock or sepsis, graft-versus-host reactions, or acute

CC inflammatory reactions. They can also be used in adjunct therapy for
 CC disease characterised by neoplastic cells that express RANK. The products
 CC can also be used for detection and drug screening.

XX
 SQ Sequence 1630 BP; 436 A; 355 C; 379 G; 460 T; 0 other;

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Quality: 1554.00 Length: 294
 Ratio: 5.304 Gaps: 0
 Percent Similarity: 99.660 Percent Identity: 99.660

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seq_documentation_block:

ID V41378 standard; cDNA; 954 BP.

XX V41378;

XX AC V41378;

XX DT 08-OCT-1998 (first entry)

XX DE NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.
 XX KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 KW immune response; inflammatory response; toxic shock; sepsis;
 KW RANKL; RANK ligand; tumour necrosis factor; TNF; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX FT CDS 1..954

XX FT /*tag= a
 XX FT /product= "human RANKL (ligand for RANK)"

XX PN WO9828426-A2.

XX PD 02-JUL-1998.

XX PF 22-DEC-1997; 97WO-US23775.

XX PR 14-OCT-1997; 97US-0064671.

XX PR 23-DEC-1996; 96US-0059978.

XX PR 07-MAR-1997; 97US-0813509.

XX PA (IMMV) IMMUNEX CORP.

XX PI Anderson DM, Galibert LJ, Maraskovsky E;

XX DR WPI; 1998-377657/32.

XX DR P-PSDB; W69957.

XX PT New isolated ligand for receptor activator of NF-kappa B - used to
 PT develop products for augmenting an immune response for inhibiting an
 PT inflammatory response and for protection of cells

XX PS Claim 25; Pages 59-60; 80pp; English.

XX This cDNA encodes a human RANKL, a ligand for the RANK (receptor
 CC activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a
 CC member of the tumour necrosis factor (TNF) family. A soluble RANK
 CC may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to
 CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
 CC used to induce maturation of dendritic cells and enhance their
 CC allo-stimulatory capacity, thereby augmenting an immune response. The
 CC soluble RANK polypeptide composition may also be used for regulating an
 CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
 CC may be useful in ameliorating negative effects of an inflammatory
 CC response that result from triggering of RANK, e.g. in treating toxic

CC shock or sepsis, graft-versus-host reactions, or acute inflammatory
 CC reactions. They can also be used in adjunct therapy for disease
 CC characterised by neoplastic cells that express RANK. RANKL polypeptides
 CC can also be used to identify inhibitors of RANK and thus inhibitors of
 CC an inflammatory response, and also for protecting RANK-expressing cells
 CC from the negative effects of chemotherapy or the presence of high levels
 CC of TNF-alpha. The products can also be used for detection and drug
 CC screening.
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748 CCAAGTTCTCATACCTCATGAAAGAGGAGAACCAACAGTATGGTCAGG 797
|||||
265 yAsnSerGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLysL 282
|||||
798 CAATTCTCAATTCATTTTATTTCCATAAACCTTGGTGGATTTTAACT 847
|||||
282 euArgAlaGlyGluLysSerIleGlnValSerAsnProSerLeuLeu 298
|||||
848 TACGGTCTGGAGAGGAATACGATCGAGGTCTCAACCCCTCTTACTG 897
|||||
299 AspProAspGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspI1 315
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898 GATCCGATCAGATGCAACATACACTTTGGGGCTTTTAAAGTTTCGAGATAT 947
|||||
315 eAsp 316
|||||
948 AGAT 951

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seq_name: /cgn2_2/gcgdata/geneseq/geneseq/NA1998.DAT:V41372

seq_documentation_block:

ID V41372 standard; cDNA; 954 BP.

XX V41372;

XX 08-OCT-1998 (first entry)

XX NF-kB receptor activator RANK ligand (RANKL) encoding cDNA.

XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;

XX Immune response; inflammatory response; toxic shock; sepsis;

XX RANKL; RANK ligand; tumour necrosis factor; TNF; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..954

XX /*tag= a

XX /product= "human RANKL (ligand for RANK)"

XX WO9828424-A2.

XX 02-JUL-1998.

XX 22-DEC-1997; 97WO-US23866.

XX 14-OCT-1997; 97US-0064671.

XX 23-DEC-1996; 96US-0059978.

XX 07-MAR-1997; 97US-0813509.

XX (IMMV) IMMUNEX CORP.

XX Anderson DM, Galibert LJ, Maraskovsky E;

XX WPI; 1998-377655/32.

XX P-PSDB; W68293.

XX New isolated receptor activator of necrosis factor-kappa B - useful
 for, e.g. developing products for regulating an immune or
 inflammatory response, treating toxic shock or sepsis

XX Example 7; Pages 59-60; 80pp; English.

XX This cDNA encodes a human RANKL, a ligand for the RANK (receptor
CC activator of necrosis factor-kappaB (NF-kB)) polypeptide. RANK is a
CC member of the tumour necrosis factor (TNF) family. Host cells transformed
CC or transfected with an expression vector comprising the RANK encoding
CC nucleic acid can be used to produce recombinant RANK protein. The soluble
CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell
CC expressing membrane-associated RANK with a soluble RANK which binds to
CC RANK ligand (RANKL). The soluble RANK polypeptide composition may also be
CC used for regulating an immune or inflammatory response. Inhibition of
CC NF-kB by RANK antagonists may be useful in ameliorating negative effects
CC of an inflammatory response that result from triggering of RANK, e.g. in
CC treating toxic shock or sepsis, graft-versus-host reactions, or acute
CC inflammatory reactions. They can also be used in adjunct therapy for
CC disease characterised by neoplastic cells that express RANK. The products
CC can also be used for detection and drug screening.

SQ Sequence 954 BP; 255 A; 239 C; 227 G; 233 T; 0 other;

alignment_scores:
Quality: 1417.50 Length: 318
Ratio: 4.709 Gaps: 2
Percent Similarity: 94.654 Percent Identity: 84.277

alignment_block:
US-08-989-362-2 x V41372 ..

Align seg 1/1 to: V41372 from: 1 to: 954

1 MetArgArgAlaSerArgAspTyrGlyLysTyrLeuArgSerSerGluG1 17
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1 ATGCGCGCGCCAGCAGAGACTACACCAAGTACCTGGCGTGGCTCGGAGGA 50

17 uMetGlySerGlyProGlyValProHisGluGlyProLeuHisProAlap 34
|||||
51 GATGGCGGGCGGCGGCGGAGCGGCGGAGGCGGCGGCGGCGGCGGCGGCGG 97

34 roSerAlaProAlaProAlaProProAlaAlaSerArgSerMetPhe 50
|||||
98 CGCGCGCGCTGGCGCGCCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 147

51 LeuAlaLeuLeuGlyLeuGlyLeuGlyGlnValValCysSerIleAlaLe 67
:::|||||
148 GTGGCCCTCTCTGGCGTGGGCGTGGGCGAGGTTCTCTGCAGCGCTCGCCCT 197

67 uPheLeuTyrPheArgAlaGlnMetAspProAsnArgIleSerGluAsps 84
|||||
198 GTTCTTCTATTTTCAGACGCGCAGATGCGATCTCTAATAGAAATATCAGAAGATG 247

84 erThrHisCysPheTyrArgIleLeuArgLeuHisGluAsnAlaGlyLeu 100
:::|||||
248 GCACCTACTGCATTTATAGAAATTTTGAGACTCCATGAAATATGCAGATTTT 297

101 GlnAspSerThrLeuGluSerGluAspThr.....LeuProAspSerCy 115
|||||
298 CAAGACACAACCTCTGGAGATCAAGATACAAATTAATACCTGATTCATG 347

115 sarArgMetLysGlnAlaPheGlnGlyAlaValGlnLysGlnLeuGlnH 132
|||||
348 TAGGAGAATTAACAGGCGCTTCAAGGAGGTGTGCAAAAGGAATTAACAAC 397

132 isIleValGlyProGlnArgPheSerGlyAlaProAlaMetMetGluGly 148
|||||
398 ATATCGTTGGATCACACACATCAGACAGAGAAAGCGATGGTGGATGGC 447

149 serTrpLeuAspValAlaGlnArgGlyLysProGlnAlaGlnProPheAl 165
|||||
448 TCATGGTTAGATCTGGCCAGAGAGGCAAGCTTGAAGCTCAGCCCTTTTGC 497

165 aHisLeuThrIleAsnAlaAlaSerIleProSerGlySerHisLysValT 182
|||||
498 TCATCTCACATTATATGCCACCGACATCCCATCTGGTTCCCATAAAGTGA 547

182 hrLeuSerSerTrpTyrHisAspArgGlyTrpAlaLysIleSerAsnMet 198
:::|||||
548 GTCCTGCTCTTGGTACCATGATCGGGGTGGGCCAAGATCTCCAACATG 597

199 ThrLeuSerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTrLe 215
|||||
598 ACTTTTAGCAATGGAAACTAATAGTTAATCAGATGGCTTTTATTACCT 647

215 uTyrAlaAsnIleCysPheArgHisGluThrSerGlySerValProt 232
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648 GTATGCCAACATTTGCTTTCGACATCATGAACCTTCAGGAGACCTAGCTA 697

232 hrAspTyrLeuGlnLeuMetValTyrValVallyThrSerIleLysIle 248
|||||
698 CAGAGTATCTCAACTAATAGTGTAGCTCAGTAAACACCATCAAAATC 747

249 ProSerSerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerG1 265
|||||
748 CCAAGTTCTCATACCTGATGAAGGAGGAAGCACCAGTATTGGTCAGG 797

265 yAsnSerGluPheHisPheTyrSerIleAsnValGlyGlyPhePhelysL 282
|||||
798 GAATTCGAATTCATTTTATTTATCCATAAACGTTGGTGGATTTTAAAGT 847

282 euArgAlaGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeu 298
|||||
848 TACGGTCTGGAGAGAAATCAGCATCGAGGTCTCCAACCCCTCCTTACTG 897

299 AspProAspGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspI1 315
|||||
898 GATCCGATTCAGATGCAACATACTTTGGGCTTTTAAAGTTCGAGATAT 947

315 eAsp 316
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948 AGAT 951

seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT:299964
seq_documentation_block:
ID: 299964 standard; DNA: 2271 BP.
XX
AC 299964;
XX
DT 25-JUL-2000 (first entry)
XX
DE DNA encoding a human osteoprotegerin ligand (OPGL).
XX
KW Osteoprotegerin ligand; OPGL; osteoprotegerin; osteoclastogenesis;
KW tumour necrosis factor receptor; type II transmembrane protein;
KW osteoclast differentiation; CSF-1; osteoclast activator;
KW immune response; osteoporosis; bone resorption; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 185..1138
FT /*tag=a
FT /product= "osteoprotegerin ligand"
XX
XX WO200015807-A1.
XX
XX 23-MAR-2000.
XX
XX 13-SEP-1999; 99WO-DK00481.
XX
XX 15-SEP-1998; 98DK-0001164.
XX 02-OCT-1998; 98US-0102896.
XX
XX (MEBI-) M & E BIOTECH AS.
XX
XX Halkier T, Haaning J;
XX

WPI; 2000-271444/23.
P-PSDB; Y84417.

In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used to treat, prevent and ameliorate osteoporosis -

Disclosure; Page 75-77; 110pp; English.

The present sequence encodes a human osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis factor receptor family, which blocks osteoclastogenesis in a dose dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are 87% homologous. OPGL is a potent osteoclast differentiation factor when combined with CSF-1. It is not capable of inducing osteoclast differentiation in the absence of CSF-1. OPGL is also an activator of mature osteoclasts. The specification describes a method for the *in vivo* down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one OPGL analogue to induce an immune response in the animal. The method and OPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive bone resorption.

Sequence 2271 BP; 658 A; 462 C; 5:12 G; 629 T; 0 other;

alignment scores:

Quality:	1417.50	Length:	318
Ratio:	4.709	Gaps:	2
Percent Similarity:	94.654	Percent Identity:	84.277

alignment_block:

08-989-362-2 x 299964

Align seg 1/1 to: Z99964 from: 1 to: 2271

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17 uMetGlySerGlyProGlyValProHisGluGlyProLeuHisProAlap 34
 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 235 GATGGGCGGGGCCCGCCGAGCCCCCGACACGPGGGCCCCCTGCAC...GCC 281

34 roSerAlaProAlaProAlaProProAlaAaLaserArgSerMetPhe 50
|| ||||||| ||||||| ||||||| |||||||
282 CGCGCGGCTGGCGGCACAGCCCCGCCGCCGTCCGTCATGTC 331

51 LeuAlaLeuLeuGlyLeuGlyClnValValCysSerIleAlaLe 67
:::|||||
332 GTGGCCCTCTCGGGGCTGGGCGAGGTGTCTGACAGCTGCCT 381

67 uPheLeuTyrPheArgAlaGlnMetAspProAsnArgILeSerGluAspS 84
 ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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84 erThrHisCysPheTrArgIleLeuArgLeuHiscLusAsnAlaGlyLeu 100
::: :::
432 GCACCTACTGCATTTATAGAAATTTTGGAGAC TCCATGAAGAATGCAGATTTT 481

101 GlnAspSerThrLeuGluSerGluAspThr.....LeuProAspSerCys 115
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482 CAAGACACAACCTCTGGAGACTCAGATACACA NAATTAATACTGTTCATG 531

115 sArgArgMetLysGlnAlaPheGlnGlyAlaValGlnLysGlnLeuGlnH 132
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 532 TAGGAGAAATAAACAGGCGCTTCAAGGAGC TGTGCAAAAGCAATTACAC 581

132 isIIeValGlyProGlnArgPheSerGlyAlaProAlaMetMetGluGlu 148
|||||
582 ATATCGTTGGATCACAGCACATCAGAGCAG AGAAGCGTGGCTGATGCG 631
|||||

149 SerTrpLeuAspValAlaGlnArqGlyLys?roGluAlaGlnPropheAl 165

632	TCATGGTTAGATCTGGCCAAAGAGGAAAGCTTGAAGCTCAGCCTTTTGC	681
165	ahisLeuThrIleAsnAlaSerIleProSerGlySerHisLysValt	182
682	TCATCTCACTATTAAATGCCACCCACATCCCATCTGGTTCCATAAAGTGA	731
182	hrLeuSerSerTrpTyrHisAspArgGlyTrpAlaLysIleSerAsnMet	198
732	GTCTGCTCTCTTGGTACCATGATCGGGTGGCCAAAGATCTCCCAACATG	781
199	ThrLeuSerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrLe	215
782	ACTTTTAGCAATGGAAACATAATAGTTAATCAGGATGGCTTTATTACCT	831
215	uTyrAlaAsnIleCysPheArqHisGluThrSerGlySerValProT	232
832	GTATGCCACATTTGCTTCGACATCATGAACATTCAGGAGACCTAGCTA	881
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882	CAGAGTATCTTCAACTAATGGTGTACGTCACTAAACACGATCAAAATC	931
249	ProSerSerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerG	265
932	CCAAGTTCATACCTCGATGAAGAGGAGGAAAGCACCAGTATTGGTCAGG	981
265	YAsnSerGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLysL	282
982	GAATCTGTAATTCATTTTATTTCATAAACGTTGGTGGATTTTTTAAGT	1031
282	euArgAlaGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeu	298
1032	TACGGCTGGAGAGAAATCAGCATCGAGGTCTCCAAACCCCTCCTTACTG	1081
299	AspProAspGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspI	315
1082	GATCCGGATCAGGATGCAACATACTTTGGGGCTTTTAAAGTTCGAGATAT	1131
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seq_documentation_block:		
ID:	V70285 standard; DNA; 2274 BP.	
XX		
AC	V70285;	
XX		
DT	11-FEB-1999 (first entry)	
XX		
DE	Human osteoprotegerin binding protein from the pcDNA/huOPGbb	
XX		
KW	Human; osteoprotegerin binding protein; OPG binding protein	
KW	osteoporosis; osteoclast maturation; bone disease; metastas	
KW	hypercalcaemia; osteoclast differentiation and activation r	
KW	Paget's disease; ss.	
XX		
OS	Homo sapiens.	
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CDS	/*tag= a	
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FT		
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PN	W09846751-A1.	
XX		
PD	22-OCT-1998.	
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XX	15-APR-1998; 98WO-US07584.	
PF		
XX		
XX	30-MAR-1998; 98US-0052521.	
PR		

PR 16-APR-1997; 97US-0842842.
 PR 23-JUN-1997; 97US-0880855.
 XX (AMGE-) AMGEN INC.
 PA Boyle WJ;
 XX
 PI
 DR WPI: 1998-594578/50.
 DR P-PSDB; W83195.
 XX
 PT Nucleic acid encoding osteoprotegerin binding protein - useful for,
 PT e.g. treating bone diseases by modulating osteoclast differentiation
 PT and for diagnosis
 XX
 PS Claim 1; Fig 4; 47pp; English.
 XX
 CC The present sequence encodes human osteoprotegerin (OPG) binding protein.
 CC Host cells transfected with vectors containing nucleic acid molecules
 CC encoding OPG binding protein are used to produce recombinant OPG binding
 CC protein. OPG binding protein is used in binding assays to determine
 CC osteoprotegerin (OG) in biological samples; to screen for specific
 CC binding agents (particularly agonists and antagonists, including
 CC intracellular proteins); to raise Ab (useful in immunoassays for
 CC detection of OPG binding protein) and to identify compounds that
 CC modulate binding of OPG binding protein to osteoclast differentiation
 CC and activation receptor (ODAR). The nucleic acid molecule encoding OPG
 CC binding protein can be used to detect OPG binding protein-encoding
 CC sequences, e.g. screening for related sequences, also to produce
 CC transgenic animal models, while complementary sequences are used for
 CC antisense regulation of OPG binding protein expression. Modulators of
 CC OPG binding protein, particularly soluble forms of OPG binding protein
 CC or Ab, are used to treat or prevent bone diseases, e.g. osteoporosis,
 CC bone loss caused by arthritis or metastases, hypercalcaemia, Paget's
 CC disease, periodontal disease, osteoporosis, loosening of prostheses,
 CC optionally in combination with agents that promote bone growth.
 XX
 SQ Sequence 2274 BP; 658 A; 463 C; 523 G; 630 T; 0 other;

alignment_scores:
 Quality: 1417.50 Length: 318
 Ratio: 4.709 Gaps: 2
 Percent Similarity: 94.654 Percent Identity: 84.277
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 US-08-989-362-2 x V70285 ..
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 17 uMetGlySerGlyProGlyValProHisGluGlyProLeuHisProAlap 34
 |||||
 235 GATGGCGCGCGCGCCAGCAGCGCCGACGAGGCGCCCTGCAC...GCC 281
 34 roSerAlaProAlaProAlaProProProAlaAlaSerArgSerMetPhe 50
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 67 uPheLeuTyrPheArgAlaGlnMetAspProAsnArgIleSerGluAsps 84
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 382 GTTCTCTATTTCAGAGCGCAGATGGATCCTAATAGATATACAGAGATG 431
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 432 GCACCTCACTGCAATTATAGAATTTTGAGACTCCATGAAATGCGAGATTTT 481

101 GlnAspSerThrLeuGluSerGluAspThr.....LeuProAspSerCy 115
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 482 CAAGACACAACTCTGGAGAGTCAAGATACAAAATAATTAATCTGATTCATG 531
 115 sArgArgMetLysGlnAlaPheGlnGlyAlaValGlnLysGluLeuGlnH 132
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 132 IsIleValGlyProGlnArgPheSerGlyAlaProAlaMetMetGluGly 148
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 582 ATATCGTTGGATCATCAGCAGCATCAGAGCAGAGAAAGCATGGTGGATGGC 631
 149 SerTrpLeuAspValAlaGlnArgGlyLysProGluAlaGlnPropheAl 165
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 832 GYATCCCAACATTTGCTTTTCGACATCATGAACCTTCAGGAGACCTAGCTA 881
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 |||||
 882 CAGAGTATCTTCACTAATGGTGTAGTCTACTATAAACACCATCAAAATC 931
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seq_name: /cgn2_2/gcdata/geneseq/geneseq/NA1998.DAT.V69887

seq_documentation_block:

ID V69887 standard; cDNA to mRNA; 954 BP.

XX

AC V69887;

XX

DT 10-FEB-1999 (first entry)

XX

DE Nucleic acid encoding a human OCIF-binding molecule (OBM).

XX

KW Osteoclastogenesis inhibitory factor; OCIF; OCIF-binding molecule; OBM;
 KW osteoclast; bone absorption factor; bone disorder; calcium metabolism;
 KW human; ss.

XX

OS Homo sapiens.

XX

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 28, 2000, 19:33:49 ; Search time 412.16 Seconds
(without alignments)
48.654 Million cell updates/sec

Title: US-08-989-362-2
Perfect score: 1675

Sequence: 1 MRRASRDYGYLRSSEMGs.....LLDPDQDQTFYGAQKVDID 316

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Total number of hits satisfying chosen parameters: 182106

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_65.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	185.5	11.1	261	2 S53090	CD40 ligand - bovi
2	183	10.9	278	2 A49266	fas ligand - rat
3	182	10.9	279	2 A53062	Fas ligand - mouse
4	173.5	10.4	281	2 I38707	Fas ligand - human
5	171.5	10.2	261	2 I53476	CD40 ligand - huma
6	157	9.4	260	2 S21738	CD40 ligand - mous
7	149	8.9	234	1 J01344	tumor necrosis fac
8	146.5	8.7	235	1 OWNSN	tumor necrosis fac
9	143.5	8.6	233	1 S22052	tumor necrosis fac
10	141	8.4	234	1 JH0529	tumor necrosis fac
11	140	8.4	233	2 S11688	tumor necrosis fac
12	139.5	8.3	233	1 QWHUN	tumor necrosis fac
13	137.5	8.2	234	1 A25451	tumor necrosis fac
14	135.5	8.1	235	2 I54490	tumor necrosis fac
15	133.5	8.0	233	1 S24642	tumor necrosis fac
16	133	7.9	185	2 S52715	tumor necrosis fac
17	133	7.9	232	1 S12606	tumor necrosis fac
18	129.5	7.7	235	2 JH0029	tumor necrosis fac
19	129.5	7.7	306	2 I49139	lymphotoxin-beta -
20	117	7.0	244	2 A46066	lymphotoxin beta -
21	115.5	6.9	193	2 S06192	tumor necrosis fac
22	103.5	6.2	340	2 S49742	hypothetical prote
23	103	6.1	3848	2 T17414	TipC protein - sli
24	99.5	5.9	558	2 T23649	hypothetical prote
25	99	5.9	440	2 I49681	glyceraldehyde-3-p
26	97	5.8	450	2 S38114	hypothetical prote
27	95.5	5.7	553	2 B55514	dihydrolipoamide S
28	94	5.6	1486	1 B40333	collagen alpha 1(I
29	93.5	5.6	205	1 QWHUX	lymphotoxin alpha

30	92.5	5.5	197	1 JH0309	tumor necrosis fac
31	92	5.5	549	2 JC5926	secreted klotho pr
32	92	5.5	785	2 T23456	hypothetical prote
33	92	5.5	1012	2 JC5925	membrane klotho pr
34	90.5	5.4	658	2 T39500	serine/threonine-s
35	90	5.4	3011	1 S40770	genome polyprotein
36	89	5.3	1694	2 S50065	sialoadhesin - mou
37	88.5	5.3	202	1 B27303	tumor necrosis fac
38	88.5	5.3	477	2 T38409	adenylyl cyclase-a
39	88.5	5.3	1547	2 JQ0096	hypothetical 176K
40	88	5.3	347	2 H75253	hypothetical prote
41	88	5.3	560	1 J01221	probable 60K inner
42	88	5.3	1420	2 T37781	probable cytoskele
43	88	5.3	2774	2 A43359	microtubule-associ
44	87	5.2	275	2 T01088	cryptophan synthas
45	87	5.2	451	2 T36149	hypothetical prote

ALIGNMENTS

RESULT 1

S53090

CD40 ligand - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999

C:Accession: S53090

R:Mertens, B.E.L.C.; Muriuki, M.

submitted to the EMBL Data Library, February 1995

A:Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.

A:Reference number: S53090

A:Accession: S53090

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-261 <MER>

A:Cross-references: EMBL:Z48469; NID:g732569; PIDN:CAA88363.1; PID:g732570

Query Match 11.1%; Score 185.5; DB 2; Length 261;
Best Local Similarity 25.1%; Pred. No. 3.3e-08;
Matches 75; Conservative 50; Mismatches 111; Indels 63; Gaps 15;

QY	32	PAPSAPAPPPAASRMFLLGLGLGVVCSIALF-LYFRAQMDPNRISDSTHCFYR	90
Db	8	PSPRSVAATGPP--VSMKIFMYLLTVFLITQMGSAFVYLHRRLD--KIEDER-----	57
QY	91	ILRLHE-----NAGLQDSTLESEDTLPSCRRMKQAFQAVOKELQHVGPORF	139
Db	58	--NLHEDFVFMKTTQRCNKGGESL--NCEIRSRFEDLVKDIMQN---REV	104
QY	140	SGAPAMMEGSLDVAQRCKPEAOPFAHLTINAAIPSGSHKVTLSNWDHRCWAKISN--	197
Db	105	KKKEKFE-----MHKGDQEPQIAAHV-----ISEASSKTTSLQWAPKGYTSLNNL	152
QY	198	MTLSNGK-LRVNQGFYLYANICF-RHHTSGSVPTDYQLMLWVYVKTISIPSSH--	253
Db	153	VTLNGKQLAVKRGFYIYTVTFCSNREPLSQP-----FIASLCLKSPGSGERI	204
QY	254	LMKGSGTKNNSGNSEFHYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDQATFYGAFKV	312
Db	205	LLRAANTH--SSSKPCGQOSIHLGGVFELQSGASVFVNVDPQSQVSHGTGFTSFGLLKL	261

RESULT 2

A49266

fas ligand - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C:Accession: A49266

R:Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.

Cell 75, 1169-1178, 1993

A:Title: Molecular cloning and expression of the Fas ligand, a novel member of the tu

A:Reference number: A49266; MUID:94084792

QY 177 GSHKVTLSWYHQRGAKISNMTLSNKLKRVNODGFYLLVYANICFRHRTSGSVPTDYLQ 236
 Db 160 -----LEWEDYGIYLLSGYKKGGLVNETGLIFVYSKVYFRGSCNN-----LP 206
 QY 237 LMVYVVKTSIKIPSSHNLMKRGSTKNMGSNEEFHYSINVGCFKLRAGEISIQVSNPS 296
 Db 207 LSHKVVYMRNSKYPDQLVME-GKMMSYCTTGQMKWARSYLGAVENLTSADHLVYNVSELS 265
 QY 297 LLDPDQDQATYFGAFKV 312
 Db 266 LVNFEESQTFGLYKL 281

RESULT 5
 I53476
 CD40 ligand - human
 N;Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
 C;Species: Homo sapiens (man)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 08-Oct-1999
 C;Accession: I53476; S28017; JH0793; S26694; S28852; S25684; S30593
 R;Gauchat, J.
 FEBS Lett. 315, 259-266, 1992
 A;Title: Human CD40-ligand: Molecular cloning, cellular distribution and regulation of e
 A;Reference number: I53476; MUID:93138085
 A;Accession: I53476
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-261 <RES>
 R;Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.;
 EMBO J. 11, 4313-4321, 1992
 A;Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for
 A;Reference number: S28017; MUID:93049181
 A;Accession: S28017
 A;Molecule type: mRNA
 A;Residues: 1-261 <HOL>
 A;Cross-references: EMBL:L07414; NID:g180123; PIDN:AAA35662.1; PID:g180124
 R;Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.
 J. Exp. Med. 176, 1543-1550, 1992
 A;Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin
 A;Reference number: JH0793; MUID:93094757
 A;Accession: JH0793
 A;Molecule type: mRNA
 A;Residues: 1-261 <SPR>
 A;Cross-references: EMBL:Z15017; NID:g38483; PIDN:CAA78737.1; PID:g38484
 R;Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T.
 J. Exp. Med. 176, 1543-1550, 1992
 A;Title: Cloning of TRAP, a ligand for CD40 on human T cells.
 A;Reference number: S26694; MUID:93076854
 A;Accession: S26694
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-261 <GRA>
 A;Cross-references: EMBL:X68550; NID:g37269; PIDN:CAA48554.1; PID:g37270
 R;Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J.
 FEBS Lett. 315, 259-266, 1993
 A;Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of e
 A;Reference number: S28852; MUID:93138085
 A;Accession: S28852
 A;Molecule type: mRNA
 A;Residues: 1-261 <GAU>
 A;Cross-references: EMBL:L07414; NID:g180123; PIDN:AAA35662.1; PID:g180124
 A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln
 C;Genetics:
 A;Gene: GDB:CD40LG; HICM1; IMD3
 A;Cross-references: GDB:120632; OMIM:308230
 A;Map position: Xq26-Xq26
 C;Keywords: glycoprotein; transmembrane protein
 F;13-44/Domain: transmembrane #status predicted <TMM>
 F;45-261/Domain: extracellular #status predicted <EXT>
 F;6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.2%; Score 171.5; DB 2; Length 261;
 Best Local Similarity 25.2%; Pred. No. 4.9e-07;
 Matches 75; Conservative 49; Mismatches 111; Indels 63; Gaps 16;

QY 33 APSAPAPAPPPAASRMFLALLGLIGLQGVVCSTALP-LYFRAQMDPNRISEDSHCFYRI 91
 Db 9 SPRSAATGLP--ISMKIFMYLLTVFLITOMIGSALEFAVYLHRRLD--KIEDER----- 57

QY 92 LRLHE-----NAGLODSTLESEDTLPDSCRRMKQAFQGVQKELQIHVGPQRFS 140
 Db 58 -NLHEDFVFMKTIQRNTGERSLSLL-----NCEIKSQEGFV-KDIM-----LN 101

QY 141 GAPAMMEGSLDVAORGKPEAOPFAHLITNAASIPSGSHKVTLSWYHQRGAKISN--M 198
 Db 102 KEETKKENSF--EMKGDQNPQIAAHV-----ISEASKTTSVLQWAEKGYTMSNNLV 153

QY 199 TILSNCK-LRVNODGFYLLVYANICF-RHHEFSGSVPTDYLQLMVYVVKTSIKIPSSH--L 254
 Db 154 TLENGKQLTVKRQGLYYIYAQVTFCSNREASSQAP-----FIASLCLKSGRFERIL 205

QY 255 MKGSTKNMGSNEFHFYSINVGCFKLRAGEISIQVSNPSLLDDPDQDQATYFGAFKV 312
 Db 206 LRAANTH--SSAKPCQQSIHLGGVFELQPGASVFVNVTDPQSVSHGTGTFSGLLKL 261

RESULT 6
 S21738
 CD40 ligand - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999
 C;Accession: S21738
 R;Armitage, R.J.; Fanslow, W.C.; Strockbine, L.; Sato, T.A.; Clifford, K.N.; Macduff,
 ; Cosman, D.; Spriggs, M.K.
 Nature 357, 80-82, 1992
 A;Title: Molecular and biological characterization of a murine ligand for CD40.
 A;Reference number: S21738; MUID:92244364
 A;Accession: S21738
 A;Molecule type: mRNA
 A;Residues: 1-260 <ARM>
 A;Cross-references: EMBL:X65453; NID:g50351; PIDN:CAA46448.1; PID:g50352
 C;Keywords: glycoprotein; transmembrane protein
 F;23-46/Domain: transmembrane #status predicted <TMM>
 F;47-260/Domain: extracellular #status predicted <EXT>
 F;239/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.4%; Score 157; DB 2; Length 260;
 Best Local Similarity 24.8%; Pred. No. 8e-06;
 Matches 75; Conservative 51; Mismatches 105; Indels 72; Gaps 16;

QY 32 PAPSAPAPAPPPAASRMFLALLGLIGL-QGVVCSTALFLYFRAQMDPNRISEDSHCFYR 90
 Db 8 PSPRSVATGLP--ASMKIFMYLLTVFLITOMIGSVLFAVYLHRRLD--KVEEE----- 56

QY 91 ILRLHE-----NAGLODSTLESEDTLPDSCRRMKQAFQGVQ-----KELQHV 134
 Db 57 -VNLHEDFVFKKLRCKNGESLSLL-----NCEEMRPFEDLVKIDITLNKE----- 103

QY 135 GQRFSGAPAMMEGSLDVAORGKPEAOPFAHLITNAASIPSGSHKVTLSWYHQRGAK 194
 Db 104 -----EKKENSF--EMQGRDEDQIAAHVSEA-----NSNAASVYLQWAKKGYTM 147

QY 195 ISNMT-LSNGK-LRVNODGFYLLVYANICF-RHHEFSGSVPTDYLQLMVYVVKTSIK--IP 249
 Db 148 KSNLVMLENGKQLTVKREGLYYYTQVTFCSNREPSRQP-----FIVGLWLKPSIG 199

QY 250 SSHNLMKGSTKNMGSNEEFHFYSINVGCFKLRAGEISIQVSNPSLLDDPDQDQATYFGA 309
 Db 200 SERILLKAANTHSSQLCEQQ--SVHLGGVFELQAGASVFVNVTASQVIHRVGFSSFGL 257

QY 310 PKV 312

Db 258 LKL 260

RESULT 7

J01344

tumor necrosis factor alpha precursor - horse

N:Alternate names: cachectin; TNF alpha

C:Species: Equus caballus (domestic horse)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C:Accession: J01344

R:Su, X.; Morris, D.D.; McGraw, R.A.

Gene 107, 319-321, 1991

A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis factor

A:Reference number: J01344; MUID:92084125

A:Accession: J01344

A:Molecule type: DNA

A:Residues: 1-234 <SU>

A:Cross-references: GB:M64087; NID:gl64244; PIDN:AAA30959.1; PID:gl64245

C:Comment: This protein is an important proximal mediator of endotoxemia.

C:Genetics:

A:Gene: TNF-alpha

A:Introns: 62/3; 79/1; 95/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane

F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>

F:19-230/Binding site: myristate (Lys) (covalent) #status predicted

F:82/Binding site: carboxylate (Ser) (covalent) #status predicted

F:146-178/Disulfide bonds: #status predicted

Query Match 8.9%; Score 149; DB 1; Length 234;

Best Local Similarity 24.1%; Pred. No. 3.2e-05;

Matches 47; Conservative 38; Mismatches 72; Indels 38; Gaps 9;

QY 133 IVGPORFSGAPAMGSLDVAQRK-----PEAQPFALHTTNAASIPSGSHKVTLSWY 187

Db 55 VIGPQREQLPNAFO-SINPLAQTLRSSRSTPSDKPVAHVAN-----PQAEGL-----QWL 106

QY 188 HDRGWAKISN-MTLNSGKLRVNQDGFYLYANICFRHHETSGSVPTDYLLQLMVYVVKTSI 246

Db 107 SGRANALLANGKLTNDQLVPLDGLYLIYSQVLEK-----GQCPSTHLLTHTISRLAV 162

QY 247 KIPSSHNLMKG-----GSTKNMGNSEHFYISYNGGFKLRAGEEISTQVSN 294

Db 163 SYPSKVNLLSAIKSPCHTESPQAEAKPW-----YEPIYLGGVFQLEKGDLSAEINQ 215

QY 295 PSLLD-PQDQATYFG 308

Db 216 PNYLDFAESGQVYFG 230

RESULT 8

QWMSN

tumor necrosis factor alpha precursor - mouse

N:Alternate names: cachectin; TNF alpha

C:Species: Mus musculus (house mouse)

C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 04-Feb-2000

C:Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36696

R:Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.

DNA 7, 193-201, 1988

A:Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis factor

A:Reference number: A22908; MUID:88224564

A:Accession: A22908

A:Molecule type: DNA

A:Residues: 1-235 <SHI>

A:Cross-references: GB:M20155

R:Shakhov, A.N.; Nedospasov, S.A.

Bloorg. Khim. 13, 701-705, 1987

A:Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucleotide sequence

A:Reference number: S03791; MUID:87298639

A:Accession: S03791

A:Molecule type: DNA

A:Residues: 1-235 <SHA>

A:Cross-references: GB:M38296; NID:g202086; PIDN:AAA40459.1; PID:g202087

A>Note: article in Russian with English abstract

R:Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.

Nucleic Acids Res. 15, 9083-9084, 1987

A:Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor necrosis factor) gene

A:Reference number: A93679; MUID:88067722

A:Accession: A27303

A:Molecule type: DNA

A:Residues: 1-235 <SEM>

A:Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68530.1; PID:g54832

R:Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V.

Proc. Natl. Acad. Sci. U.S.A. 82, 6050-6064, 1985

A:Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necrosis factor

A:Reference number: A25164; MUID:85298296

A:Accession: A25164

A:Molecule type: mRNA

A:Residues: 1-235 <PEN>

A:Cross-references: GB:M11731; NID:g202084; PIDN:AAA40458.1; PID:g202085

R:Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashima, E.

Nucleic Acids Res. 13, 4417-4429, 1985

A:Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic expression

A:Reference number: A23127; MUID:85242112

A:Accession: A23127

A:Molecule type: mRNA

A:Residues: 1-235 <FRA>

A:Cross-references: GB:X02611; NID:g54844; PIDN:CAA26457.1; PID:g54845

R:Cseh, K.; Beutler, B.

J. Biol. Chem. 264, 16256-16260, 1989

A:Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide results in two distinct mature proteins

A:Reference number: A34251; MUID:89380231

A:Accession: A34251

A:Molecule type: protein

A:Residues: 70-87 <CSE>

R:Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.

Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986

A:Title: Identification of a common nucleotide sequence in the 3'-untranslated region of the murine TNF gene

A:Reference number: I59058; MUID:86149365

A:Accession: I59058

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-230, 'R', 232-235 <RES>

A:Cross-references: GB:M13049; NID:g202082; PIDN:AAA40457.1; PID:g202083

R:Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.

Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990

A:Title: Characterization of high molecular weight glycosylated forms of murine tumor necrosis factor

A:Reference number: A36696; MUID:91097531

A:Accession: A36696

A:Molecule type: protein

A:Residues: 80-85, 'X', 87-99 <SHE>

C:Genetics:

A:Introns: 62/3; 81/1; 97/1

A>Note: the first intron occurs in the 5'-untranslated region

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane

F:80-235/Product: tumor necrosis factor #status experimental <MAT>

F:20/Binding site: myristate (Lys) (covalent) #status predicted

F:84/Binding site: carboxylate (Ser) (covalent) #status predicted

F:86/Binding site: carboxylate (Asn) (covalent) #status predicted

F:148-179/Disulfide bonds: #status predicted

Query Match 8.7%; Score 146.5; DB 1; Length 235;

Best Local Similarity 25.6%; Pred. No. 5.3e-05;

Matches 51; Conservative 36; Mismatches 67; Indels 45; Gaps 11;

QY 133 IVGPORF-----SGAP-----AMMEGSLDVAQRKPEAQPFALHTTNAASIPSGSHKVTLS- 184

Db 55 VIGPQREKPEPNGLPLISSMAQTTLRSSNSND-KPVAHVAN-----HOVEQL 105

QY 185 SWYHGRWAKISN-MTLNSGKLRVNQDGFYLYANICFRHHETSGSVPTDYLLQLMVYVVK 243

Db 106 EWLSQLANALLANGMDLKNQLVVPADGLYLVYVQVLEK-----GQCPDIV-LLTHVTS 159

QY 244 -----TSIKIPSHNLMKGGSTKNWSEHFHYSINVGFFKLRAGEETSI 290
Db 160 RFAISVQEKVNNLSAVAKSPCKDTPGEALKPW-----YEPIYLGGVFOLEKGDQLSA 212
QY 291 QVSNPSLLD-PDQDQATYFG 308
Db 213 EVNLPKYLDAESGQVYFG 231
RESULT 9
S22052
tumor necrosis factor alpha precursor - baboon
C:Species: Papio sp. (baboon)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: S22052
R:Sanjanwala, M.; Edwards, A.
A:Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
A:Reference number: S22052
A:Accession: S22052
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <SAS>
A:Cross-references: EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160
C:Genetics:
A:Introns: 62/3; 78/1; 94/1
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F:19,20/Binding site: myristate (Lys) (covalent) #status predicted
F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:145-177/Disulfide bonds: #status predicted
Query Match 8.6%; Score 143.5; DB 1; Length 233;
Best Local Similarity 25.6%; Pred. No. 9.3e-05;
Matches 50; Conservative 36; Mismatches 70; Indels 39; Gaps 11;
QY 133 IVGPQR-FSGAPAMMEGSLDVAQRK---PEAQPPAHITINAAISPGSHKVTLSWY 187
Db 55 VIGPQREEFKDPSLI--SPLAQAVRSSSTPSPDKPVAHVAN---PQAEGLD---QWL 105
QY 188 HDRGWAKISN-WTLNGLRVNODGGFYLYANICFRHHEHSGSVPTDYQLQ-----M 238
Db 106 NRRANALLANGVELRNQNLVVPSEGLYLYSQVLFK---GQGPCSTHVLTTHTISRIAV 161
QY 239 VYVVK---TSIKIPSHNLMKGGSTKNWSEHFHYSINVGFFKLRAGEETSIQVSN 294
Db 162 SYOTKVNLLSAIKSPQRETPEGAELKPW-----YEPIYLGGVFOLEKGDRLSAEINL 214
QY 295 PSLLD-PDQDQATYFG 308
Db 215 PDYLDFAESGQVYFG 229
RESULT 10
JH0529
tumor necrosis factor alpha precursor - sheep
N:Alternate names: cachectin; TNF alpha
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: JH0529; S48118; S13114; S20661
R:Green, I.R.; Sargan, D.R.
Gene 109, 203-210, 1991
A:Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with
A:Reference number: JH0529; MUID:92112044
A:Accession: JH0529
A:Molecule type: mRNA
A:Residues: 1-234 <GRE>
A:Cross-references: EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406
A:Experimental source: alveolar macrophage
R:Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.
Immunol. Cell Biol. 69, 273-283, 1991

A:Title: Molecular cloning, expression and characterization of ovine TNF-alpha.
A:Reference number: S48118; MUID:92155784
A:Accession: S48118
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-234 <NAS>
A:Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807
R:Young, A.J.; Hay, J.B.; Chan, J.Y.C.
Nucleic Acids Res. 18, 6723, 1990
A:Title: Primary structure of ovine tumor necrosis factor alpha cDNA.
A:Reference number: S13114; MUID:91067496
A:Accession: S13114
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-62,64-234 <YOU>
A:Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404
A:Note: comparison with the introns of homologous sequences suggest that this is prob
C:Superfamily: tumor necrosis factor
C:Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lym
F:1-77/Domain: propeptide #status predicted <PRO>
F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F:20/Binding site: myristate (Lys) (covalent) #status predicted
F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:96/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:146-178/Disulfide bonds: #status predicted

Query Match 8.4%; Score 141; DB 1; Length 234;
Best Local Similarity 25.8%; Pred. No. 0.00015;
Matches 51; Conservative 31; Mismatches 72; Indels 44; Gaps 11;
QY 133 IVGPQR-FSGAPAMMEGSLDVAQRKPEAQPPAHITINAAISPG---SHKVTLSWYH 188
Db 55 VIGPQREEQSPA-----GPSENRPLVQ-TLRSSQASNNKPVAVHVNISAPG 101
QY 189 DRGWA-KTSMNLSNG-KLRVQ-----DGFYLYANICFRHH-----ETSGSVP 231
Db 102 QLRMGDSYANALMANGVELKNQNLVVPDGLYLYSQVLFGRHGCGPSTPLFTHITSRIA 161
QY 232 TDYQLQMVYVVKTSIKIPSHNLMKGGSTKNWSEHFHYSINVGFFKLRAGEETSIQ 291
Db 162 VSY-QTKVNIL-SAIKSPCHRETLEGAELKPW-----YEPIYQGVFOLEKGDRLSAE 212
QY 292 VSNPSLLD-PDQDQATYFG 308
Db 213 INLPYLDYAESGQVYFG 230 .

RESULT 11
S11688
tumor necrosis factor alpha precursor - cat
C:Species: Felis silvestris catus (domestic cat)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Feb-2000
C:Accession: S11688
R:McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.; Rawlings, C.A.
Nucleic Acids Res. 18, 5563, 1990
A:Title: Gene sequence of feline tumor necrosis factor alpha.
A:Reference number: S11688; MUID:91016860
A:Accession: S11688
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <MCG>
A:Cross-references: EMBL:X54000; NID:g1084; PIDN:CAA37948.1; PID:g295777
C:Genetics:
A:Introns: 62/3; 78/1; 94/1
C:Superfamily: tumor necrosis factor
C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F:19,20/Binding site: myristate (Lys) (covalent) #status predicted
F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:145-177/Disulfide bonds: #status predicted
Query Match 8.4%; Score 140; DB 2; Length 233;

A25451

tumor necrosis factor alpha precursor - rabbit
N:Alternate names: cachectin; TNF alpha
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: A25454; A25451; J50727
R:Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H.
DNA 5, 149-156, 1986
A:Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rabbit tumor necrosis factor alpha
A:Reference number: A25454; MUID:86219711
A:Accession: A25454
A:Molecule type: mRNA
A:Residues: 1-234 <ITO>
A:Cross-references: GB:M12845; NID:gl65759; PIDN:AAA31486.1; PID:gl65760
R:Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
DNA 5, 157-165, 1986
A:Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
A:Reference number: A25451; MUID:86219712
A:Accession: A25451
A:Molecule type: DNA
A:Residues: 1-234 <IT2>
A>Note: This sequence differs from that shown in having a Gln inserted between residues R:Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990
A:Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF- α and TNF- β
A:Reference number: JH0309; MUID:91065534
A:Accession: J50727
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-62, 'O', 63-234 <SHA>
A:Cross-references: GB:M60340; GB:M35326; NID:gl65754; PIDN:AAA31484.1; PID:gl65756
C:Genetics:
A:Introns: 62/3; 80/1; 96/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; member of TNF family
F:1-81/Domain: propeptide #status predicted <PRO>
F:82-234/Product: tumor necrosis factor #status predicted <MAT>
F:19,20/Binding site: myristate (Lys) (covalent) #status predicted
F:83/Binding site: carboxylate (Ser) (covalent) #status predicted
F:147-178/Disulfide bonds: #status predicted

Query Match 8.2%; Score 137.5; DB 1; Length 234;
Best Local Similarity 22.6%; Pred. No. 0.0003;
Matches 68; Conservative 31; Mismatches 99; Indels 103; Gaps 12;

QY 27 EGPLPAPSAPAPPPAASR-----SMFLALLGLGQVVCISIALFLYFRAQMDPNRIS 81
DB 14 EGPL-----PKAGGPGQSKRCICLSFSLVAGATTLLFC-----LLHFRVIGPQEEES 63
QY 82 EDSTHCFYRILRLHENAGLDQSTLESEDLPDSCRRMKQAFQAVOKELQHIIVGPQRFSG 141
DB 64 PNNHLV-----NPVAQWVTLRS-----ASRALSDKPLAHVV----- 95
QY 142 APAMEGSWLDVAQRKPEAQAFAHLTINAASIPSGSHKVTLSWYHDGWAKISN-MTL 200
DB 96 ANPQVEGQ-----LQWLSQRANALLANGMKL 121
QY 201 SNGKLRVNDQGFYLLYANICFRHHETSGSVPTDYQLQMLVYVVTSTKIPSSHNLKMG--- 257
DB 122 TONQLVVPADGLLYYSQVLF-----SGQCRSYVLLTHTVSRFAVSYPKNVLLSAIKS 176
QY 258 -----GSTKNWGSNEFEHYSINVGFFKLRAGEEISIOVSNPSLLD-PDQATYF 307
DB 177 PCHRETPAEAPMAW-----YEPIYLGGVFQLEKGRDRLSTVENQPEYLDLAESGVYF 229
QY 308 G 308

DB 230 G 230

RESULT 14

154490

tumor necrosis factor alpha precursor - white-footed mouse
C:Species: Peromyscus leucopus (white-footed mouse)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000
C:Accession: 154490
R:Crew, M.D.; Filipowsky, M.E.
Immunogenetics 35, 351-353, 1992

A:Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus l
A:Reference number: 154490; MUID:92218012
A:Accession: 154490
A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA
A:Residues: 1-235 <RES>
A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507

C:Genetics:

A:Gene: TNF

A:Introns: 62/3; 81/1; 97/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation

F:19,20/Binding site: myristate (Lys) (covalent) #status predicted

F:84/Binding site: carboxylate (Ser) (covalent) #status predicted

Query Match 8.1%; Score 135.5; DB 2; Length 235;
Best Local Similarity 25.1%; Pred. No. 0.00044;
Matches 51; Conservative 31; Mismatches 68; Indels 53; Gaps 10;

QY 133 IVGPQRFSGAP-----AMMEGSLDVAQRKPEAQAFAHLTINAASIPSGSHKVTLS 185
DB 55 VIGPQREKFPNNLPIIGSMAQTLTLRSSQNSD-KPVAHVAN-----HQVDEQL 105

QY 186 WYHRGWAKISNMTLSNG-KURVNO-----DGYYLYANICFRHHETSGSVPTDYQLQMV 239
DB 106 EWSLRG-----ANALLANGMDLKNQLVIPADGLYLVYSQVLFKGGCQSYV-----LLT 155

QY 240 YVVK-----TSIKPSSHNLKMGSTKNWGSNEFEHYSINVGFFKLRAGE 286
DB 156 HTVSRFAVSIEDKVNLLSAIKSPCKPTEGSELKPW-----YEPIYLGGVFQLEKGD 208

QY 287 EISIQVSNPSLLD-PDQATYF 308
DB 209 RLSAEVNLPKYLDFAESGVYF 231

RESULT 15
S24642

tumor necrosis factor alpha precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000

C:Accession: 146047; S24642

R:Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.

Cytokine 5, 336-341, 1993

A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and
A:Reference number: 146046; MUID:94083525

A:Accession: 146047

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-233 <CL2>

A:Cross-references: EMBL:Z14137; NID:g796; PIDN:CAA78511.1; PID:g798

C:Genetics:

A:Gene: TNFA

A:Introns: 62/3; 78/1; 94/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein

F:20/Binding site: myristate (Lys) (covalent) #status predicted

F:81/Binding site: carboxylate (Ser) (covalent) #status predicted

F:145-177/Disulfide bonds: #status predicted

Query Match 8.0%; Score 133.5; DB 1; Length 233;
Best Local Similarity 25.8%; Pred. No. 0.00064;
Matches 51; Conservative 30; Mismatches 72; Indels 45; Gaps 11;

RESULT 14

QY 133 IVGPQR--FSGAPAMMEGSLDVAQRKPEA---QPAHLTINAASIPSGSHKVTLS 187


```
Db 55 VIGQREESPGPSI--NSPLVQTLRSSQASSNKPVAHVAD-----INSPG 100
Qy 188 HDRGWAKISNMTLSNG-KLRVNQ-----DGFYLYANICFRHH-----ETSGSVP 231
Db 101 QLRWDSYANALMANGVKLEDNQLVVPADGLYLIYSQVLFRCQGCSTPLFLTHTISRIA 160
Qy 232 TDYLOLMVYVVKTSIKIPSSHNLMKGGSTKNWGNSEPHFYSINVGGPFKLRAGEEISIQ 291
Db 161 VSY-QTKVNIL-SAIKSPCHRETPEWAEAKPW-----YEPIYOGGVFQLEKGDRLSAE 211
Qy 292 VSNPSLLD-PDODATYFG 308
Db 212 INLPDYLDYAESGOVYFG 229
```

Search completed: December 29, 2000, 08:33:43
Job time: 46794 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 28, 2000, 19:38:36 ; Search time 231.76 Seconds
(without alignments)
43.560 Million cell updates/sec

Title: US-08-989-362-2
Perfect score: 1675
Sequence: 1 MRRASRDYKGLRSSEMGs.....LLDPDQATYCAFKVQDID 316

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	258.5	15.4	281	1 TRAI_HUMAN	P50591 homo sapien
2	244	14.6	291	1 TRAI_MOUSE	P50592 mus musculus
3	185.5	11.1	261	1 TNF5_BOVIN	P51749 bos taurus
4	183	10.9	278	1 FASL_RAT	P36940 rattus norv
5	182	10.9	279	1 FASL_MOUSE	P41047 mus musculus
6	173.5	10.4	281	1 FASL_HUMAN	P48023 homo sapien
7	171.5	10.2	261	1 TNF5_HUMAN	P29965 homo sapien
8	157	9.4	234	1 TNFA_CAVPO	P51435 cavia porce
9	137	9.4	260	1 TNF5_MOUSE	P27548 mus musculus
10	149	8.9	234	1 TNFA_HORSE	P29553 equus cabal
11	148.5	8.9	233	1 TNFA_MACFA	P79337 macaca fasc
12	147.5	8.8	233	1 TNFA_MACMU	P48094 macaca mula
13	146.5	8.7	235	1 TNFA_MOUSE	P06804 mus musculus
14	143.5	8.6	233	1 TNFA_PAPHU	O77510 papio hamad
15	143.5	8.6	233	1 TNFA_PAPSP	P33620 papio sp. (
16	141	8.4	234	1 TNFA_SHEEP	P23383 ovis aries
17	140	8.4	233	1 TNFA_FELCA	P19101 felis silve
18	139.5	8.3	233	1 TNFA_CANFA	P51742 canis fami
19	139.5	8.3	233	1 TNFA_HUMAN	P01375 homo sapien
20	137	8.2	235	1 TNFA_RABIT	P04924 oryctolagus
21	135.5	8.1	235	1 TNFA_PERLE	P36939 peromyscus
22	133.5	8.0	233	1 TNFA_BOVIN	P06599 bos taurus
23	133	7.9	232	1 TNFA_PIG	P23563 sus scrofa
24	129.5	7.7	233	1 TNFA_MARMO	O35734 marmota mon
25	129.5	7.7	235	1 TNFA_RAT	P16599 rattus norv
26	129.5	7.7	306	1 TNFC_MOUSE	P41155 mus musculus
27	128	7.6	229	1 TNFA_CEREL	P51743 cervus elap
28	117	7.0	244	1 TNFC_HUMAN	O06643 homo sapien
29	115.5	6.9	193	1 TNFA_CAPHI	P13296 capra hircu
30	109.5	6.5	233	1 TNFA_MACEU	O77764 macropus eu
31	103.5	6.2	340	1 YMD1_YEAST	Q03703 saccharomyc
32	99	5.9	440	1 G3PT_MOUSE	O64467 mus musculus
33	97	5.8	450	1 YK22_YEAST	P36135 saccharomyc

34	95.5	5.7	553	1 ODP2_ALCEU	Q59098 alcaligenes
35	93.5	5.6	205	1 TNFB_HUMAN	P01374 homo sapien
36	92.5	5.5	197	1 TNFB_RABIT	P10154 oryctolagus
37	90.5	5.4	658	1 PAK1_SCHPO	P50527 schizosacch
38	89	5.3	1694	1 SN_MOUSE	Q62230 mus musculus
39	88.5	5.3	202	1 TNFB_MOUSE	P09225 mus musculus
40	88.5	5.3	477	1 CAP2_HUMAN	P40123 homo sapien
41	88.5	5.3	559	1 GL6S_CAPHI	P50426 capra hircu
42	88.5	5.3	1547	1 RRPO_PMV	P20951 papaya mosa
43	88	5.3	560	1 60IM_PSEPU	P25754 pseudomonas
44	88	5.3	2774	1 MAPA_RAT	P34926 rattus norv
45	85	5.1	304	1 NKR9_HUMAN	Q14953 homo sapien

ALIGNMENTS

RESULT 1					
TRAI_HUMAN					
ID	TRAI_HUMAN	STANDARD;	PRT;	281 AA.	
AC	P50591;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	TNF-RELATED APOPTOSIS INDUCING LIGAND (TRAIL PROTEIN) (APO-2 LIGAND)				
DE	(APO-2L).				
GN	TNFSF10 OR TRAIL OR APO2L.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 96111955.				
RA	Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,				
RA	Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,				
RA	Goodwin R.G.;				
RT	"Identification and characterization of a new member of the TNF				
RT	family that induces apoptosis.";				
RL	Immunity 3:673-682(1995).				
RN	(2)				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-PLACENTA;				
RA	MEDLINE; 96278649.				
RA	Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A.,				
RA	Ashkenazi A.;				
RT	"Induction of apoptosis by Apo-2 ligand, a new member of the tumor				
RT	necrosis factor cytokine family.";				
RL	J. Biol. Chem. 271:12687-12690(1996).				
CC	-1- FUNCTION: INDUCES APOPTOSIS.				
CC	-1- SUBUNIT: HOMOTRIMER (POTENTIAL).				
CC	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).				
CC	-1- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG				
CC	AND PROSTATE.				
CC	-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.				
CC	-----				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; U37518; AAC50332.1; -				
DR	EMBL; U57059; AAB01233.1; -				
DR	MIN; 603598; -				
DR	INTERPRO; IPR000478; -				
DR	PFAM; PF00229; TNF; 1.				
DR	PROSITE; PS00251; TNF_1; 1.				
DR	PROSITE; PS50049; TNF_2; 1.				
KW	Cytokine; Transmembrane; Signal-anchor; Apoptosis.				
FT	DOMAIN 1 17				
FT	TRANSMEM 18 38				
FT	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).				

FT DOMAIN 39 281 EXTRACELLULAR (POTENTIAL).
SQ SEQUENCE 281 AA; 32509 MW; DDAAAF78DAAB2F6D CRC64;
Query Match 15.4%; Score 258.5; DB 1; Length 281;
Best Local Similarity 26.4%; Pred. No. 2.5e-14;
Matches 78; Conservative 54; Mismatches 113; Indels 51; Gaps 10;
Qy 43 PAASRMFLALGLGLGQVCSIALFLYFRAQMD--PNRISDSTHCFYRLRHENAGL 100
Db 10 PSLGTCVLIVFTVLLQSLCVAVYVYFTNELKQMDKYSGIACF-----LKEDDSY 64
Qy 101 QDSTLESDTLDPDCRRMKQAFQAVOK-----ELQHVGPQRFSGAPAMM 146
Db 65 WDP--NDESNMSPQVQKWLRLVRKMLRTSEETISTVQEQNISP----- 113
Qy 147 EGSWLDVAQRKPEAQPFPAHLT-----INAAISIPSGSHKVTL-----SSWYHDR-GWAKIS 196
Db 114 -----VREPGQVAV--AHITGTRGNTLSSPKSKKEKALGRKINSWESSRSGHSPLS 165
Qy 197 NMTLSNGKLRVNDQGFYLYANICFRHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMK 256
Db 166 NLHLRNGELVIEHKGFIYISQTYERFOEIKENTKNDQVMQYIYKYT-SYDPDPILLMK 224
Qy 257 GGSTKNWGSNFEHYSINVGFFKLRAAGEEISIOVSNPSLLDPDODATYFGAFV 312
Db 225 SARNCSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLMDMDEASFFGAFLV 280
RESULT 2
TRAIL_MOUSE STANDARD; PRT; 291 AA.
AC P50592;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TNF-RELATED APOPTOSIS INDUCING LIGAND (TRAIL PROTEIN).
GN TNFSF10 OR TRAIL.
OS Mus, musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96111955.
RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA Goodwin R.G.
RT Identification and characterization of a new member of the TNF
family that induces apoptosis.
RL Immunity 3:673-682(1995).
CC -!- FUNCTION: INDUCES APOPTOSIS.
CC -!- SUBUNIT: HOMOTRIMER (POTENTIAL).
CC -!- TISSUE SPECIFICITY: WIDESPREAD.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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or send an email to license@isb-sib.ch).
CC EMBL; U37522; AAC52345.1; -.
DR MGD; MGI:107414; TRAIL.
DR INTERPRO; IPR000478; -.
DR PFAM; PF00229; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Transmembrane; Signal-anchor; Apoptosis.
FT DOMAIN 1 17
FT TRANSMEM 18 38
FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

FT DOMAIN 39 291 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 52 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 291 AA; 33477 MW; 3FEACAB9F0D7D802 CRC64;
Query Match 14.6%; Score 244; DB 1; Length 291;
Best Local Similarity 27.5%; Pred. No. 4.1e-13;
Matches 83; Conservative 50; Mismatches 111; Indels 58; Gaps 15;
Qy 52 ALGLGLGQ-----VCSIAL-----FLYFRAQMD--PNRISDSTHCFYRIL 92
Db 6 ALKDLFSQHFRRMVICIVLLVLLQAVSVAVYMYFTNEMKQLQDNYSKIGLACFSK-- 63
Qy 93 RLHENAGLQDSTLESDTLDPDC-----RRMKQAFQCAVQKELQHVIG--PQRFSGAPAMM 146
Db 64 ---TDEDFWDST--DGEILNRPCLOVKRQLYQLIEEVTLRFTQDTISTVPEKQLSTPLP 118
Qy 147 EGSWLDVAQRKPEAQPFPAHLT-----INAAISIPSGSHKVTL-----SSWYHDR-GWAKIS 196
Db 119 RG-----GRPO-KVAAHITGTRNSALIPISKDGTLOGKIESWESSRSGHSFLN 169
Qy 197 NMTLSNGKLRVNDQGFYLYANICFRHETSGSVPTDYL---QLMVYVVKTSIKIPS 250
Db 170 HVLFRNGELVIEHKGFIYISQTYERFOEIKENTKNDQVMQYIYKYT-SYDPD 228
Qy 251 SHNLKGGSTKNWGSNFEHYSINVGFFKLRAAGEEISIOVSNPSLLDPDODATYFGAF 310
Db 229 PIVLMSKARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLMDLQDEASFFGAF 288
Qy 311 KV 312
Db 289 LI 290
RESULT 3
TNFS_BOVIN STANDARD; PRT; 261 AA.
AC P51749;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CD40 LIGAND (TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL ANTIGEN
GP39).
GN TNFSF5 OR CD40LG OR CD40L.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96006582.
RA Mertens B.E.L.C., Muriuki M., Gaidulis L.;
RT Cloning of two members of the TNF-superfamily in cattle: CD40 ligand
and tumor necrosis factor alpha.
RL Immunogenetics 42:430-431(1995).
CC -!- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
STIMULUS AS WELL AS ICE PRODUCTION IN THE PRESENCE OF IL-4.
CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING (BY SIMILARITY).
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC EMBL; Z48469; CAA88363.1; -.

DR	HSP; P29965; ITALY.
DR	INTERPRO; IPR000478; -
DR	PFAM; PF00229; TNF_1;
DR	PROSITE; PS00251; TNF_1; 1.
DR	PROSITE; PS50049; TNF_2; 1.
KW	Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT	DOMAIN 1 22
FT	TRANSMEM 23 46
FT	
FT	DOMAIN 47 261
FT	DISULFID 178 218
FT	CARBOHYD 240 240
FT	
SQ	SEQUENCE 261 AA; 29242 MW; 8491FEFB30A787ED CRC64;
Query Match 11.1%; Score 185.5; DB 1; Length 261;	
Best Local Similarity 25.1%; Pred.No 2.4e-08;	
Matches 75; Conservative 50; Mismatches 111; Indels 63; Gaps	
QY	32 PAPSAPAPAPPAAASRMFLALGLGLGQGVCSIALF-LYFRAQMDPNRISDSTHCFYR 90
DB	8 PPSRVATGPP--VSMKIFMYLLTVFLITQMIGSALFAVYLVHRLD--KIEDER----- 57
QY	91 ILRLHE-----NAGLDSTLESDTLPDSCRHKQAFQAGAVQELQHIIVGPQRF 139
DB	58 --NLHEDFVPMKTIQRCKNGEGSLSL-----NCEIIRSFEDLVKDIMON---KEV 104
QY	140 SGAPAMMEGSLDVAORGPPEAOPFAHLITNAASIPSGSHKVTLSWYHDCGWAQTSN-- 197
DB	105 KKEKNFE-----MKGQDEQPTAAHV-----ISEASKTTSVLQWAPKGYTYLSNML 152
QY	198 MTLNNGK-LRVNDGDFYIYANICF-RHNETGSVPTDYLQLMVYVVKTSIKIPSSH-- 253
DB	153 VTLENGKQLAVKRGFYIYIVQVTFCSNRETLQAP-----FIASCLKSPSGSRI 204
QY	254 LMKGGSTKNWGSNEPHFYSINVGVEFKLRAGEETISQVNSPSLDDPDODATYGAQKV 312
DB	205 LLRAANTH--SSSKPCQCGSIHLGGVFELQSGASVEFVNTDPSQVSHGTGFTSFGLLKL 261
RESULT 4	
FASL_RAT STANDARD; PRT; 278 AA.	
ID	FASL_RAT
AC	P36940;
DT	01-JUN-1994 (Rel. 29, Created)
DT	01-JUN-1994 (Rel. 29, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	FAS ANTIGEN LIGAND.
GN	TNFSF6 OR APTILG1 OR FASL.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN	[1]
RE	SEQUENCE FROM N.A.
RA	MEDLINE; 94084792.
RA	Suda T., Takahashi T., Golstein P., Nagata S.;
RT	"Molecular cloning and expression of the Fas ligand, a novel member
RT	of the tumor necrosis factor family.";
RL	Cell 75:1169-1178(1993).
CC	-1- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
CC	TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CC	CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
CC	FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
CC	PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
CC	T CELLS, OR BOTH.
CC	-1- SUBUNIT: HOMOTRIMER (PROBABLE).
CC	-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
CC	INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
CC	SURFACE.
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND
CC	THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES
CC	KIDNEY AND LUNG.
CC	-1- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.

```

CC  -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL: U03470; AAC52129.1; -.
CC  INTERPRO: IPR000478; -.
CC  PFAM: PF00229; TNF; 1.
CC  PROSITE: PS00251; TNF_1; 1.
CC  PROSITE: PS50049; TNF_2; 1.
CC  Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis.
CC  DOMAIN 1 77
CC  TRANSMEM 78 99
CC  FT DOMAIN 100 278
CC  FT DOMAIN 4 69
CC  FT DOMAIN 45 58
CC  FT DISULFID 199 230
CC  FT CARBOHYD 116 116
CC  FT CARBOHYD 247 247
CC  FT CARBOHYD 257 257
CC  SQ SEQUENCE 278 AA; 31140 MW; 2898E18A862CEAC6 CRC64;
CC  -----
CC  Query Match 10.9%; Score 183; DB 1; Length 278;
CC  Best Local Similarity 23.4%; Pred. No. 4.2e-08;
CC  Matches 75; Conservative 42; Mismatches 107; Indels 96; Gaps 13;
CC  -----
CC  QY 14 SSEEMSGS-----PGVPHEGGLHPAPAPAPAP-----PAASRSMFTALL 54
CC  Db 34 SSGRPGGQRRPPPPPPPPGL-PPPSQPPPLPLSPKKKDNIELMPLVFFMVLV 92
CC  QY 55 GLGLGQVVCSTALFLYFRAQMDPNRISDSETHCFYRILRLHENAGLQDSTLESDDTLPS 114
CC  Db 93 GMGLG-----MYQLFHLQKELAELEFNTNH-----SLRVSSFEKQIANPST 133
CC  QY 115 CRRMKQAFQAGVAKELQIHVGPQFSGAPAMWESSWLDVAQRGKPEAQPFAHLTIN--AA 172
CC  Db 134 PSETK-----KPRSS--VAHLTGNPRSR 153
CC  QY 173 SPSGSHKVTLSWYHDRGWAKISNMTLSNGKLRVNODGFYLYVANTICFRHETSGSVPT 232
CC  Db 154 SIP-----LEWEDTYGALISGVYKKYKGLVINEAGLYFVYSKVYFR-GQSCNQ- 203
CC  QY 233 DYLOLMVYVKTSTIKIPSSHNLMKGGSTKNWGSNEFFHYSINVGGFFKLRAGEISIQV 292
CC  Db 204 --LSHKVYM--RNFKYPGDLVLM-EKKLVYCTGTQIWAHSSYLGAVFNLTVDHLVNI 258
CC  QY 293 SNPSLLDPDQDAYFGAFKV 312
CC  Db 259 SQSLINFEESKTFFGLYKL 278
CC  -----
CC  RESULT 5
CC  FASL_MOUSE STANDARD; PRT; 279 AA.
CC  ID FASL_MOUSE
CC  AC P41047; Q61217;
CC  DT 01-FEB-1995 (Rel. 31, Created)
CC  DT 01-FEB-1995 (Rel. 31, Last sequence update)
CC  DT 15-JUL-1999 (Rel. 38, Last annotation update)
CC  DT FAS ANTIGEN LIGAND.
CC  GN TNFSF6 OR APTLIG OR FASL OR GLD.
CC  OS Mus musculus (Mouse).
CC  OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC  OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC  [1]
CC  RN SEQUENCE FROM N.A.
CC  RX MEDLINE; 94185175.
CC  RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,

```

RA Suda T., Nagata S.;
 RT "Generalized lymphoproliferative disease in mice, caused by a point
 mutation in the Fas ligand.";
 RL Cell 76:969-976(1994).
 RN [2].
 RP SEQUENCE FROM N.A., AND 3D-STRUCTURE MODELING.
 RC STRAIN=C57BL/6;
 RX MEDLINE: 95388076.
 RA Peitsch M.J., Tschopp J.J.;
 RT "Comparative molecular modelling of the Fas-ligand and other members
 of the TNF family.";
 RL Mol. Immunol. 32:761-772(1995).
 RN [3].
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95196085.
 RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
 RT Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
 RL "The mouse Fas-ligand gene is mutated in gld mice and is part of a
 TNF family gene cluster.";
 RN Immunity 1:131-136(1994).
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/C;
 RA Fenner M.H., Shioda T., Isselbacher K.J.;
 RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in
 two amino acids.";
 RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
 RN [5].
 RP CHARACTERIZATION OF VARIANT GLD.
 RX MEDLINE: 96091792.
 RA Hahne M., Peitsch M.C., Imler M., Schroeter M., Lowin B.,
 RT Rousseau M., Bron C., Renno T., French L., Tschopp J.;
 RL "Characterization of the non-functional Fas ligand of gld mice.";
 Int. Immunol. 7:1381-1386(1995).
 CC -1- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
 TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
 CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
 CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
 PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
 T CELLS, OR BOTH.
 CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
 INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
 SURFACE.
 CC -1- DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED
 LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE
 RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL: U06948; AAA17800.1; -
 DR EMBL: U10984; AAA19778.1; -
 DR EMBL: S76752; AAB33780.1; -
 DR EMBL: U58995; AAB02915.1; -
 DR HSSP: P01375; 2TUN.
 DR MGD: MGI:99255; FASL.
 DR INTERPRO: IPR000478; -
 DR PFAM: PF00229; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis;
 KW Disease mutation.
 FT DOMAIN 1 78 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 79 100 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
 FT DOMAIN 101 279 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 4 69 PRO-RICH.

FT DOMAIN 45 51 POLY-PRO.
 FT DISULFID 200 231 BY SIMILARITY.
 FT CARBOHYD 117 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 184 184 T -> A (IN STRAIN BALB/C).
 FT VARIANT 218 218 E -> G (IN STRAIN BALB/C).
 FT VARIANT 273 273 F -> L (IN GLD; ABOLISH BINDING OF FASL TO
 ITS RECEPTOR).
 SQ SEQUENCE 279 AA; 31442 MW; 37972E2728E0A1CA CRC64;
 Query Match 10.9%; Score 182; DB 1; Length 279;
 Best Local Similarity 22.7%; Pred. No. 5.1e-08;
 Matches 72; Conservative 48; Mismatches 105; Indels 92; Gaps 13;
 QY 13 RSSEEMSGCGVPHGPHLHAPSAPAPP-----PAASRMFLALIGLG 57
 Db 38 RGPDRRRPPPPPPVSP-LPPSQPLPLPLTLPLKKDHTNLMLPVVFFMVLVGMG 96
 QY 58 LGQVCSIALFLYFRAQMDPNRISDSTHCFYRLRLHFNAGLQDSTLESDTLPDSCRR 117
 Db 97 LG-----MYQLFHLQKE---LAE-----LREFTNQSLKVSFEKQIANPST--- 134
 QY 118 MKOAFQGVQKELQHVGPORFSGAPAMMEGSLDVAQRGKPEAQPFALHTIN--AASIP 175
 Db 135 -----PSE-----KKEPRSVAHLTGNPHSRISIP 157
 QY 176 SGSHKVTLSWYHGRGWAKISNMTLSNGKLRVQDQGFYLYANICFRHHETSGSVPTDYL 235
 Db 158 -----LEWEDTYGTALISGVYKKGGLVINETGLYFYVSKYVYFR--GOSCNQPLNH- 207
 QY 236 QLMVYVKTSIKIPSSHNLMKMGSTKNWGSSEHFYSINVGPFKLRAGEEISIQVSNP 295
 Db 208 --KVYM--RNSKYPEDLVLMW-EKRLNYCTTGQIWAHSSYLGAVENLTSDADHLYVNISQL 262
 QY 296 SLDDPPQDATYFGAFKV 312
 Db 263 SLINFEESKTFEGLYKL 279
 RESULT 6
 FASL_HUMAN STANDARD; PRT; 281 AA.
 ID FASL_HUMAN
 AC P48023;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL).
 GN TNFSF6 OR APTLIG1 OR FASL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95105731.
 RA Alderson M.;
 RT "Fas ligand mediates activation-induced cell death in human T
 lymphocytes.";
 RL J. Exp. Med. 181:71-77(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95127560.
 RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
 RT "Human Fas ligand: gene structure, chromosomal location and species
 specificity.";
 RL Int. Immunol. 6:1567-1574(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Schaeuble C.E., Poehmann R., Philippsen P., Eibel H.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]

RA Shimadzu M., Terasaki H., Ninomiya R., Shimizu S., Nunoi H.,
 RA Matsuda I.; (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 116-261.
 RX MEDLINE; 96131874.
 RA Karpusas M., Hsu Y.-M., Wang J.-H., Thompson J., Lederman S.,
 RA Chess L., Thomas D.;
 RT "2-A crystal structure of an extracellular fragment of human CD40
 RT ligand.";
 RL Structure 3:1031-1039(1995).
 RN [8]
 RP 3D-STRUCTURE MODELING OF COMPLEX WITH CD40.
 RX MEDLINE; 98266353.
 RA Singh J., Garber E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
 RA Zheng Z., Naismith J.H., Thomas D.;
 RT "The role of polar interactions in the molecular recognition of CD40L
 RT with its receptor CD40.";
 RL Protein Sci. 7:1124-1135(1998).
 RN [9]
 RP VARIANTS HIGM1 ARG-36 AND GLY-140.
 RX MEDLINE; 93156839.
 RA Korthauer U., Graf D., Mages H.W., Briere F., Padayachee M.,
 RA Malcolin S., Ugazio A.G., Notarangelo L.D., Levinsky R.J.,
 RA Kroczej R.A.;
 RT "Defective expression of T-cell CD40 ligand causes X-linked
 RT immunodeficiency with hyper-IgM.";
 RL Nature 361:539-541(1993).
 RN [10]
 RP VARIANTS HIGM1 GLU-123.
 RX MEDLINE; 93156840.
 RA Disanto J.P., Bonnefoy J.Y., Gauchat J.F.M., Fischer A.,
 RA de Saint Basile G.;
 RT "CD40 ligand mutations in x-linked immunodeficiency with hyper-IgM.";
 RL Nature 361:541-543(1993).
 RN [11]
 RP VARIANTS HIGM1 PRO-155; ASP-211 AND VAL-227.
 RX MEDLINE; 93174270.
 RA Allen R.C., Armistage R.J., Conley M.E., Rosenblatt H., Jenkins N.A.,
 RA Copeland N.G., Bedell M.A., Edelfoff S., Distche C.M.,
 RA Simoneaux D.K., Fanslow W.C., Belmont J.W., Spriggs M.K.;
 RT "CD40 ligand gene defects responsible for X-linked hyper-IgM
 RT syndrome.";
 RL Science 259:990-993(1993).
 RN [12]
 RP VARIANTS HIGM1 ALA-126; ARG-140 AND GLU-144.
 RX MEDLINE; 95233436.
 RA Macchi P., Villa A., Strina D., Sacco M.G., Morali F., Brugnani D.,
 RA Giliani S., Mantuano E., Fasth A., Andersson B., Zegers B.J.M.,
 RA Cavagni G., Reznick I., Levy J., Zan-Bar I., Porat Y., Airol P.,
 RA Plebani A., Vezzoni P., Notarangelo L.D.;
 RT "Characterization of nine novel mutations in the CD40 ligand gene in
 RT patients with X-linked hyper IgM syndrome of various ancestry.";
 RL Am. J. Hum. Genet. 56:898-906(1995).
 RN [13]
 RP VARIANTS HIGM1 PRO-155 AND VAL-227, AND VARIANT ARG-219.
 RX MEDLINE; 96133533.
 RA Lin Q., Rohrer J., Allen R.C., Larche M., Greene J.M., Shigeoka A.O.,
 RA Gatti R.A., Derauf D.C., Belmont J.W., Conley M.E.;
 RT "A single strand conformation polymorphism study of CD40 ligand.
 RT Efficient mutation analysis and carrier detection for X-linked hyper
 RT IgM syndrome.";
 RL J. Clin. Invest. 97:196-201(1996).
 RN [14]
 RP VARIANTS HIGM1 ARG-36; CYS-140; SER-231; MET-254 AND GLY-227 DEL.
 RX MEDLINE; 97295077.
 RA Nonoyama S., Shimadzu M., Toru H., Seyama K., Nunoi H., Neubauer M.,
 RA Yata J.-I., Och H.D.;
 RT "Mutations of the CD40 ligand gene in 13 Japanese patients with
 RT X-linked hyper-IgM syndrome.";
 RL Hum. Genet. 99:624-627(1997).
 CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
 CC STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE OF IL-4.

CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
 CC -1- SUBUNIT: HOMOTRIMER.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
 CC EXTRACELLULAR SOLUBLE FORM.
 CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+
 CC T-LYMPHOCYTES.
 CC -1- DISEASE: DEFECTS IN CD40LG ARE THE CAUSE OF AN X-LINKED
 CC IMMUNODEFICIENCY WITH HYPER-IGM (HIGM1), AN IMMUNOGLOBULIN ISOTYPE
 CC SWITCH DEFECT CHARACTERIZED BY ELEVATED CONCENTRATIONS OF SERUM
 CC IGM AND DECREASED AMOUNTS OF ALL OTHER ISOTYPES. AFFECTED MALES
 CC PRESENT AT AN EARLY AGE (USUALLY WITHIN THE FIRST YEAR OF LIFE)
 CC RECURRENT BACTERIAL AND OPPORTUNISTIC INFECTIONS, INCLUDING
 CC PNEUMOCYSTIS CARINII PNEUMONIA AND INTRACTABLE DIARRHEA DUE TO
 CC CRYPTOSPORIDIUM INFECTION. DESPITE SUBSTITUTION TREATMENT WITH
 CC INTRAVENOUS IMMUNOGLOBULIN, THE OVERALL PROGNOSIS IS RATHER POOR,
 CC WITH A DEATH RATE OF ABOUT 10% BEFORE ADOLESCENCE.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
 CC -1- DATABASE: NAME=CD40Lbase;
 CC NOTE=EUROPEAN CD40L DEFECT DATABASE (MUTATION DB);
 CC WWW="HTTP://WWW.EXPASY.CH/CD40LBASE/";
 CC FTP="FTP://FTP.EXPASY.CH/DATABASES/CD40LBASE";
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD154 entry;
 CC WWW="HTTP://WWW.NCBI.NLM.NIH.GOV/PROW/CD/CD154.HTM".
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 CC -----
 CC EMBL; X68550; CAA48554.1; -
 CC EMBL; X15017; CAA78737.1; -
 CC EMBL; X787878; CAA48077.1; -
 CC EMBL; L07414; AAA35662.1; -
 CC EMBL; D31797; BAA06599.1; -
 CC EMBL; D31793; BAA06599.1; JOINED.
 CC EMBL; D31794; BAA06599.1; JOINED.
 CC EMBL; D31795; BAA06599.1; JOINED.
 CC EMBL; D31796; BAA06599.1; JOINED.
 CC PIR; S25684; S25684.
 CC PIR; S26694; S26694.
 CC PIR; S28017; S28017.
 CC PIR; S28852; S28852.
 CC PIR; JH0793; JH0793.
 CC PDB; IALY; 17-SEP-97.
 CC MIM; 308230; -
 CC INTERPRO; IPR000478; -
 CC PFAM; PF00229; TNF_1; -
 CC PROSITE; PS00251; TNF_1; 1.
 CC PROSITE; PS00049; TNF_2; 1.
 CC Cytokine; transmembrane; Glycoprotein; Signal-anchor; 3D-structure;
 CC Disease mutation; Polymorphism.
 CC DOMAIN 1 22
 CC TRANSMEM 23 46
 CC CYTOPLASMIC (POTENTIAL).
 CC SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC POTENTIAL.
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC M -> R (IN HIGM1).
 CC /FTid=VAR_007513.
 CC A -> E (IN HIGM1).
 CC /FTid=VAR_007514.
 CC V -> A (IN HIGM1).
 CC /FTid=VAR_007515.
 CC SE -> RG (IN HIGM1).
 CC /FTid=VAR_007516.
 CC W -> C (IN HIGM1).
 CC /FTid=VAR_007517.
 CC W -> G (IN HIGM1).
 CC /FTid=VAR_007518.
 CC W -> R (IN HIGM1).

```
Query Match      10.2%; Score 171.5; DB 1; Length 261;
Best Local Similarity 25.2%; Pred. No. 3.5e-07;
Matches 75; Conservative 49; Mismatches 111; Indels 63; Gaps 16;

QY 33 APSAPAPPPAASRMFALLGLGQVVCIALF-LYFRAQMDPNRISDSTHCFYRI 91
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 9 SPASATGLP--ISMKIFVLLVFLITQMGSAFVYLHRLD--KIDER----- 57
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 92 LRLHE-----NAGLDSTLSEEDTLPDCRRMKQAFQAVGAKELQHVGPORFS 140
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 58 -NLHEDFVEMKTIQRCTGERSLL-----NCEIKSQFEGV-KDIM-----LN 101
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 141 GAPAMEGSWLDVAQRKPEAQAFAHLTNAASIPSGSHKVTLSWYHDRGWAKISN--M 198
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 102 KEETKKNSEF--EMQGDQNPQIAAHV-----ISEASSKTTSLQWAEKGYTMSNLY 153
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
QY 199 TISNGK-LRVNODGFYLVANICF-RHETSGVPTDYQLQMLVNVVKTISKIPSSHN--L 254
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 154 TLENGQLVVKROGLYIYAQVTFCSNREASSQAP-----FIASLCLKSGRFRERIL 205
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 255 MKGGSTKNWGSNEFFHYSINVGFFKLRAGEEISIQVSNPSLLDPDQDHYFCAEKV 312
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 206 LRAANTH--SSAKPCQSQSHLGGVPELOPGASVFVNVDPSQVSHGTGFTSGLLKL 261
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
TNFA_CAVPO STANDARD; PRT; 234 AA.
AC P51435:
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNF OR TNFA.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HARTLEY; TISSUE=LUNG;
RA Yuan H.T., Kelly F.J., Bingle C.D.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-DUNKIN-HARTLEY;
RX MEDLINE; 97462215.
RA White A.M., Yoshimura T., Smith A.W., Westwick J., Watson M.L.;
RT "Airway inflammation induced by recombinant guinea pig tumor necrosis
   factor-alpha.";
RL Am. J. Physiol. 273:L524-L530(1997).
CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
   WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
   CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
   CACHEXIA, IT IS A POTENT PROGEN CAUSING FEVER BY DIRECT ACTION
   OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
   CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
   CONDITIONS.
CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
   EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
   PROTEOLYTIC PROCESSING (BY SIMILARITY).
CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
   CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
   AND MALNUTRITION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC -----
DR EMBL; U39839; AAB06492.1; -.
DR EMBL; U77036; AAB19210.1; -.
DR HSP; P01375; 2TUN.
DR INTERPRO; IPR000478; -.
DR INTERPRO; IPR002959; -.
DR PFAM; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCR0SISFCT.
DR PRINTS; PR01235; TNFALPHA.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
FT PROPEP 1 79 BY SIMILARITY.
FT CHAIN 80 234 TUMOR NECROSIS FACTOR.
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DISULFID 147 178 BY SIMILARITY.
FT SEQUENCE 234 AA; 25793 MW; 7272C940393E7E9B CRC64;
SQ
Query Match      9.4%; Score 157; DB 1; Length 234;
Best Local Similarity 26.1%; Pred. No. 4.7e-06;
Matches 54; Conservative 26; Mismatches 65; Indels 62; Gaps 9;

QY 133 IVGPOR---FSGAPAMEGSWLDVAQRKPEAQ-----PPAHLTINAASIP 175
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :
Db 55 VIGPQREQFSSGPPF-----RPLAQTLTSLRSASQNDNDKPVAVHVAQAAE 102
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 176 SGSHKVTLSWYHDRGWAKISN-WTLSNGKLRVNODGFYLVANICFRHETSGSVPTDY 234
   | | | | | | | | | | | | | | | | | | | | | | | | :
Db 103 E-----LWLSKRANALLANGMLSDNQLVPSDGLYLYISQVLFK-----GQCPSY 150
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 235 LQLMVYVVKTSIKIPSSHNLM-----KGSSTKNWGSNEFFHYSINVGFFKL 282
   | | | | | : : : : : | | | | | | | | | | | | | | :
Db 151 LLLHTVSLRAVSYPEKVNLLSAKSPCQKETPEAERKPW-----YEIYLGCVFOL 203
   : : : : : : : : : : | | | | | | | | | | | | | | :
QY 283 RAGEEISIQVSNPSLLD-PDQDATYFG 308
   : : : : : : : : | | | | | | | | | | | | | | :
Db 204 QKGDRLSAEVLNLPQYLDFAQSGQIYFG 230

RESULT 9
TNF5_MOUSE STANDARD; PRT; 260 AA.
AC P27548:
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CD40 LIGAND (TNF-RELATED ACTIVATION PROTEIN) (TRAP) (T CELL ANTIGEN
   GP39).
DE TNFSF5 OR CD40LG OR CD40L.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92244364.
RA Amittage R., Fanslow W., Sato T.A., Clifford K.N., Strockbine L.,
RA Macduff B.M., Anderson D.M., Gimpe S.D., Davis-Smith T.,
RA Maliszewski C.R., Clark E.A., Smith C.A., Grabstein K.H., Cosman D.,
RA Spriggs M.K.;
RT "Molecular and biological characterization of a murine ligand for
   CD40.";
RL Nature 357:80-82(1992).
RN [2]
RP SIMILARITY TO THE TNF FAMILY.
RX MEDLINE; 92310561.
RA Farrah T., Smith C.A.;
RT "Emerging cytokine family.";
RL Nature 358:26-26(1992).
RN [3]
RP 3D-STRUCTURE MODELING OF 115-260.
```


RX MEDLINE; 93200072.
 RA Peitsch M.C., Jongeneel C.V.;
 RT "A 3-D model for the CD40 ligand predicts that it is a compact trimer
 similar to the tumor necrosis factors.";
 RL Int. Immunol. 5:233-238(1993).
 CC -1- FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSENCE OF CO-
 STIMULUS AS WELL AS ICE PRODUCTION IN THE PRESENCE OF IL-4.
 CC INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
 CC -1- SUBUNIT: HOMOTRIMER.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
 EXTRACELLULAR SOLUBLE FORM.
 CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+
 T-LYMPHOCYTES.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X65453; CAA46448.1; -;
 DR PIR; S21738; S21738.
 DR PDB; LCDA; 31-OCT-93.
 DR MGD; MGI-88337; TNFSF5.
 DR INTERPRO; IPR000478; -;
 DR PFAM; PF00229; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 DR CYTOKINE; Transmembrane; Glycoprotein; Signal-anchor; 3D-structure.
 FT DOMAIN 1 22
 FT TRANSMEM 23 46
 FT SIGNAL-ANCHOR (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT DISULFID 177 217
 FT CARBOHYD 239 239
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 260 AA; 29396 MW; 7E0F34F7473668B7 CRC64;

Query Match 9.4%; Score 157; DB 1; Length 260;
 Best Local Similarity 24.8%; Pred. No. 5.4e-06;
 Matches 75; Conservative 51; Mismatches 105; Indels 72; Gaps 16;
 QY 32 PAPSAPAPPAASRSMFLALLGLGL-QGVVCSTALFLYFRAQMDPNRISDSTHCYR 90
 DB 8 PPSRSVATGLP--ASMKIFMYLLTVFLITQMTGSLVFAVYLHRLD--KVEEE----- 56
 QY 91 ILRLHE-----NAGLDQDSTLESDTLDPDCRRMKQAFQAVQ-----KELQHV 134
 DB 57 -VNLHEDVFFIKKRCNKGESLSLL-----NCEMRROFEDLVKDTLNKE----- 103
 QY 135 GPQRFSGAPAMMEGSLDVAQKGPAPQAFHILTINAASIPSGSHKVTLSWYHGRGMAK 194
 DB 104 -----EKKENSF--EMQRGDEDPQIAHVVSEA-----NSAASVLQWAKKGYITM 147
 QY 195 ISNMT-LSNGK-LRVNQDGFYLYANICF-RHETSGSVPTDYQLQMLVYVVTSTK--IP 249
 DB 148 KSNLVMLENGKOLTVKREGLYVYVTVTFCNSNRPESSQRP-----PIVGLWLKPSIG 199
 QY 250 SSHNLKMGSTKNWGSNEFEHYSINVGFFKLRAGEEISIOVNSPSLLDPDQDATYFCA 309
 DB 200 SERILLKANTHSSQOLCEQ--SVHLGGVFELQAGASVFNVTASQVHRHVGFSFGL 257
 QY 310 FKV 312
 DB 258 LKL 260
 RESULT 10
 TNFA_HORSE
 ID TNFA_HORSE STANDARD; PRT; 234 AA.

P29553;
 01-APR-1993 (Rel. 25, Created)
 01-APR-1993 (Rel. 25, Last sequence update)
 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
 GN TNF OR TNFA.
 OS Equus caballus (Horse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92084125.
 RA Su X., Morris D.D., McGraw R.A.;
 RT "Cloning and characterization of gene TNF alpha encoding equine tumor
 necrosis factor alpha";
 RL Gene 107:319-321(1991).
 CC -1- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
 WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
 CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
 CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
 OR BY STIMULATION OF INTERLEUKIN 1 SECRETION. IT CAN STIMULATE
 CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
 CONDITIONS.
 CC -1- SUBUNIT: HOMOTRIMER.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
 EXTRACELLULAR SOLUBLE FORM.
 CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
 PROTEOLYTIC PROCESSING.
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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 CC -----
 DR EMBL; M64087; AAA30959.1; -;
 DR PIR; J01344; J01344.
 DR HSP; P01375; ITNF.
 DR INTERPRO; IPR000478; -;
 DR INTERPRO; IPR002959; -;
 DR PFAM; PF00229; TNF; 1.
 DR PRINTS; PR01234; TNECROSISFCT.
 DR PRINTS; PR01235; TNFALPHA.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.
 KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
 FT PROPEP 1 77
 FT CHAIN 78 234
 FT TRANSMEM 36 56
 FT DISULFID 146 178
 FT BY SIMILARITY.
 SQ SEQUENCE 234 AA; 25469 MW; E79ACE91143DF373 CRC64;
 Query Match 8.9%; Score 149; DB 1; Length 234;
 Best Local Similarity 24.1%; Pred. No. 2.2e-05;
 Matches 47; Conservative 38; Mismatches 72; Indels 38; Gaps 9;
 QY 133 IVGPQRFSGAPAMMEGSLDVAQKGM-----PEAQFAHILTINAASIPSGSHKVTLSWY 187
 DB 55 VIGPQREQLPNAFQ-SINPLAQTLRSSRTPSKPAHVAVN-----PQAEGL---QWL 106
 QY 188 HDRGWAKISN-MTSLNGKLRVNDGFFYYLYANICFRHETSGSVPTDYQLQMLVYVVTSTI 246
 DB 107 SGRANALLANGVKLTQNLVPLDGLYLVSVLFK----GQCGPSTHVLTHHTISRLAV 162
 QY 247 KIPSSHNLKMG-----GSTNWSGNSFEHYSINVGFFKLRAGEEISIQVSN 294
 DB 163 SYPSKVNLLSAIKSPCHTESPEQAEAKPW-----YEPIYLGGVFQLEKGDQLSAEINQ 215
 QY 295 PSLLD-PDQDATVFG 308

[illegible]

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Query Match      8.8%; Score 147.5; DB 1; Length 233;
Best Local Similarity 25.6%; Pred. NO. 2.9e-05;
Matches 50; Conservative 38; Mismatches 66; Indels 39; Gaps 11;

QY 133 IVGPQR--FSGAPAMEGSWLDVAORGK---PEAOPFAHLTTNAASIPSGSHKVTLSSHY 187
DB 55 VIGPQREFPKPSLI--SPLAQAVRSSRTPSDKPVAVHVN---PQAEQGL---QWL 105
QY 188 HDRGWAKISN-WTLSNGKLRVNODGFYVLYANICFRHHETSGSVPTDYLLQL-----M 238
DB 106 NRRANALLANGVELTDNQLVPSSEGLIYSQVLEK---GOGCPSNVHLLTHTSRIAY 161
QY 239 VYVK-----TSIKPSSHNLKMGSTKNSGNSEFHFYSINVGFFKLRAGEEISIQVSN 294
DB 162 SVQTVNLLLSAISKPCQRETPEGAEPKW-----YEPYILGGVFOLEKGRDLSAEINL 214
QY 295 PSLLD-PPQDATYFG 308
DB 215 PDYLDFAESGQVYFG 229

RESULT 13
TNFA_MOUSE
ID TNFA_MOUSE STANDARD; PRT: 235 AA.
AC P06804; Q62326;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNF OR TNFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88224564.
RA Shirai T., Shimizu N., Shiojiri S., Horiguchi S., Ito H.;
RT "Cloning and expression in Escherichia coli of the gene for mouse
RL tumor necrosis factor.";
RN DNA 7:193-201(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85298296.
RA Pennica D., Hayflick J.S., Bringham T.S., Palladino M.A.,
RA Goeddel D.V.;
RT "Cloning and expression in Escherichia coli of the cDNA for murine
RL tumor necrosis factor.";
RN Proc. Natl. Acad. Sci. U.S.A. 82:6060-6064(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86149365.
RA Caput D., Beutler B., Hartog K., Thayer R., Brown-Shimer S.,
RA Cerami A.;
RT "Identification of a common nucleotide sequence in the
RL 3'-untranslated region of mRNA molecules specifying inflammatory
RT mediators.";
RN Proc. Natl. Acad. Sci. U.S.A. 83:1670-1674(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85242112.
RA Fransen L., Mueller R., Marmenout A., Tavernier J., van der Heyden J.,
RA Kawashima E., Chollet A., Tizard R., van Heuverswyn H., van Vliet A.,
RA Ruyschaert M.-R., Fiers W.;
RT "Molecular cloning of mouse tumour necrosis factor cDNA and its
RL eukaryotic expression.";
RN Nucleic Acids Res. 13:4417-4429(1985).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87298639.
RA Shakhov A.N., Nedospasov S.A.;
RT "Molecular cloning of genes coding for tumor necrosis factor.
RL Complete nucleotide sequence of the genome copy of TNF-alpha in
RN mice.";
RL Bioorg. Khim. 13:701-705(1987).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88067722.
RA Semon D., Kawashima E., Jongeneel C.V., Shakhov A.N., Nedospasov S.A.;
RT "Nucleotide sequence of the murine TNF locus, including the TNF-alpha
RL (tumor necrosis factor) and TNF-beta (lymphotoxin) genes.";
RN Nucleic Acids Res. 15:9083-9084(1987).
RN [7]
RP SEQUENCE FROM N.A.
RX STRAIN-CTS, AND NOD;
RX MEDLINE; 96013654.
RA Ikegami H., Makino S., Yamato E., Kawaguchi Y., Ueda H., Sakamoto T.,
RA Takekawa K., Ogihara T.;
RT "Identification of a new susceptibility locus for insulin-dependent
RL diabetes mellitus by ancestral haplotype congenic mapping.";
RN J. Clin. Invest. 96:1936-1942(1995).
RN [8]
RP SEQUENCE OF 80-99.
RX MEDLINE; 91097531.
RA Sherry B., Juc D.-M., Zentella A., Cerami A.;
RT "Characterization of high molecular weight glycosylated forms of
RL murine tumor necrosis factor.";
RN Biochem. Biophys. Res. Commun. 173:1072-1078(1990).
RN [9]
RP SEQUENCE OF 70-87.
RX MEDLINE; 89380231.
RA Cseh K., Beutler B.;
RT "Alternative cleavage of the cachectin/tumor necrosis factor
RL propeptide results in a larger, inactive form of secreted protein.";
RN J. Biol. Chem. 264:16256-16260(1989).
RN [10]
RP IDENTIFICATION OF MEMBRANE-BOUND FORM.
RX MEDLINE; 88165056.
RA Krieger M., Perez X., Defay K., Albert I., Lu S.D.;
RT "A novel form of TNF/cachectin is a cell surface cytotoxic
RL transmembrane protein: ramifications for the complex physiology of
TNF.";
RL Cell 53:45-53(1988).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS) OF 80-235.
RX MEDLINE; 99190964.
RA Baeyens K.J., De Bondt H.L., Raeymaekers A., Fiers W., De Ranter C.J.;
RT "The structure of mouse tumour-necrosis factor at 1.4 A resolution:
RL towards modulation of its selectivity and trimerization.";
CC Acta Crystallogr. D 55:772-778(1999).
CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC -----
CC EMBL; U06950; AAA18594.1; -
DR
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DR EMBL; M13049; AAA40457.1; -
DR EMBL; M11731; AAA40458.1; -
DR EMBL; Y00467; CAA68530.1; -
DR EMBL; X02611; CAA26457.1; -
DR EMBL; M20155; AAA40462.1; ALT_SEQ.
DR EMBL; M38296; AAA40459.1; -
DR EMBL; D84196; BAA19512.1; -
DR EMBL; D84194; BAA19512.1; JOINED.
DR EMBL; D84195; BAA19512.1; JOINED.
DR EMBL; D84199; BAA19513.1; -
DR EMBL; D84197; BAA19513.1; JOINED.
DR EMBL; D84198; BAA19513.1; JOINED.
DR PIR; A23127; QWMSN.
DR PIR; A22908; A22908.
DR PIR; A25164; A25164.
DR PIR; A27303; A27303.
DR PIR; A34251; A34251.
DR PIR; S03791; S03791.
DR PDB; 2TNF; 12-OCT-99.
DR MGD; MGI:104798; TNF.
DR INTERPRO; IPR000478; -.
DR INTERPRO; IPR002959; -.
DR PFAM; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRINTS; PR01235; TNFALPHA.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;
KW 3D-structure.
FT PROPEP 1 79
FT CHAIN 80 235 TUMOR NECROSIS FACTOR.
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DISULFID 148 179
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .).
FT CONFLICT 231 231 G -> R (IN REF. 3 AND 4).
SQ SEQUENCE 235 AA; 25895 MW; 16DD2A9676D68C5D CRC64;

Query Match 8.7%; Score 146.5; DB 1; Length 235;
Best Local Similarity 25.6%; Pred. No. 3.5e-05;
Matches 51; Conservative 36; Mismatches 67; Indels 45; Gaps 11;

QY 133 IVGPQR---SCAP---AMEGSWLDVAQRGKPEAQPFAHLTINAASIPSGSHKVTLS- 184
DB 55 VIGPQRDEKFNGLPLISSMAQTLTIRSSQNSSD-KPAHVAVN-----HQVEEQ 105

QY 185 SWYHDKWAKISN-MTSLNGKLRVNDGFFLYLANICFRHHTSGSVPTDYLOLMVYVK 243
DB 106 EWLQSRANALLANGMDLKNQLVVPADGLYLYVSVLFK-----GQCCPDYV-LLHTVS 159

QY 244 -----TSIKIPSSHNLKMGSTKMWGNSGFHYFISYNGGFFKLRAGEEISI 290
DB 160 REAISYQKRVNLLSAVKSPCKDTPGAEALKPW-----YEPILGGVFQLEKGDLSA 212

QY 291 QVSNPSLLD-PQDATYFG 308
DB 213 EYNLPKYLDFAESGGQVYFG 231

RESULT 14
TNFA_PAPHU
ID TNFA_PAPHU STANDARD; PRT; 233 AA.
AC 077510;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNF OR TNFA.
OS Papio hamadryas ursinus (Chacma baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
RN [1]

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SEQUENCE FROM N.A.
RX MEDLINE: 98147379.
RA Haudek S.B., Redl H., Schlag G., Giroir B.P.;
RT "Complementary DNA (cDNA) sequence of baboon tumor necrosis factor
  alpha.";
RL Mol. Immunol. 34:1041-1042(1997).
CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
  WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
  CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
  CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
  OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
  CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
  CONDITIONS.
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
  EXTRACELLULAR SOLUBLE FORM.
CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
  PROTEOLYTIC PROCESSING.
CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
  CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
  AND MALNUTRITION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF019963; AAC31675.1; -
CC INTERPRO; IPR000478; -.
CC INTERPRO; IPR002959; -.
CC PFAM; PF00229; TNF; 1.
CC PRINTS; PR01234; TNECROSISFCT.
CC PRINTS; PR01235; TNFALPHA.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
FT PROPEP 1 76 BY SIMILARITY.
FT CHAIN 77 233 TUMOR NECROSIS FACTOR.
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DISULFID 145 177 BY SIMILARITY.
SQ SEQUENCE 233 AA; 25658 MW; B9403255058D4A03 CRC64;

Query Match 8.6%; Score 143.5; DB 1; Length 233;
Best Local Similarity 25.1%; Pred. No. 6.1e-05;
Matches 49; Conservative 38; Mismatches 69; Indels 39; Gaps 11;

QY 133 IVGPQR--FSGAPAMMEGSLDVAQRGK---PEAQPFAHLTINAASIPSGSHKVTLSWY 187
DB 55 VIGPQREFFPKDPSLI--SPLAQAVRSSRTPSPDPVHVAVN----PQAEQQL---QWL 105

QY 188 HDRGWAKISN-MTSLNGKLRVNDGFFLYLANICFRHHTSGSVPTDYLOL-----M 238
DB 106 NRRANALLANGVELTDNQLVVPSEGLYLYISQVLFK----GQCCPSNHVLLTHTISRIAV 161

QY 239 VYVVK-----TSIKIPSSHNLKMGSTKMWGNSGFHYFISYNGGFFKLRAGEEISQVSN 294
DB 162 SYQTKVNLLSAISKPCQRETPEGAEPW-----YEPILGGVFQLEKGRLSAEINL 214

QY 295 PSLLD-PQDATYFG 308
DB 215 PDYLDFAESGGQVYFG 229

RESULT 15
TNFA_PAPSP
ID TNFA_PAPSP STANDARD; PRT; 233 AA.
AC P33620;
DT 01-FEB-1994 (Rel. 28, Created)

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Search completed: December 29, 2000, 09:04:18
Job time: 48342 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 28, 2000, 19:38:02 ; Search time 601.22 Seconds
(without alignments)
49.077 Million cell updates/sec

Title: US-08-989-362-2
Perfect score: 1675
Sequence: 1 MRRASRDYGYLRSSEWGS.....LLDPDQDATYGFAPKVQDID 316

Scoring table: BLOSOM62

Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 297973

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_14.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mnc.*
- 8: sp_organalle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1675	100.0	316	11	O35235 mus musculus
2	1646.5	98.3	313	11	Q9r1y0 mus musculus
3	1417.5	84.6	317	4	O14788 homo sapien
4	164	9.8	260	6	O97605 felis silve
5	154	9.2	260	6	O97626 canis famli
6	149	8.9	234	6	Q9rTJ3
7	148	8.8	232	11	O35853
8	146.5	8.7	239	11	Q9QYH9
9	145	8.7	260	11	O922V2
10	145	8.7	260	11	Q9R254
11	142	8.5	232	4	Q9U1V3
12	140	8.4	174	4	O95150
13	139	8.3	234	6	Q28320
14	134.5	8.0	240	4	O43557
15	133.5	8.0	233	6	O18779
16	133	7.9	157	4	O43647
17	132	7.9	149	6	O97543
18	131	7.8	149	6	O97538
19	131	7.8	149	6	Q9rTg8

20	130.5	7.8	240	4	O75476
21	130	7.8	216	11	O70332
22	126.5	7.6	250	6	Q9xt47
23	123.5	7.4	138	6	Q9ttg7
24	120.5	7.2	150	6	Q9TSV8
25	109	6.5	201	6	Q9xt48
26	103	6.1	3848	5	O76737
27	102.5	6.1	225	11	O54907
28	102	6.1	169	11	O9WV90
29	99.5	5.9	558	5	O45692
30	97	5.8	325	5	Q9V5G2
31	96	5.7	1486	13	Q91717
32	95	5.7	1012	4	Q9UEF7
33	94	5.6	891	1	O93635
34	93	5.6	93	6	Q9TTJ2
35	92	5.5	294	2	O53921
36	92	5.5	549	4	Q9Y4F0
37	92	5.5	785	5	O9XUS7
38	92	5.5	1012	4	Q9UEI9
39	91.5	5.5	205	4	Q9UKS8
40	91	5.4	616	4	Q9UBP0
41	90.5	5.4	750	10	Q9Z008
42	90	5.4	355	5	O3VG08
43	90	5.4	556	12	Q9WNB6
44	90	5.4	3011	12	Q03463
45	88	5.3	347	2	Q9RR94

ALIGNMENTS

RESULT 1

O35235 PRELIMINARY; PRT; 316 AA.
AC O35235: O35306;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE TNF-RELATED ACTIVATION-INDUCED CYTOKINE (RANKL) (TRANCE) (OPGL)
DE (OSTEOPROTEGERIN LIGAND) (TUMOR NECROSIS FACTOR LIGAND) (OSTEOCLAST
DE DIFFERENTIATION FACTOR) (ODF).
GN TNFSF11 OR RANKL OR TRANCE OR OPGL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=HYBRIDOMA;
RX MEDLINE; 97460112.
RA Wong B.R., Rho J., Arron J., Robinson E., Orlinick J., Chao M.,
RA Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA Choi Y.;
RT "TRANCE is a novel ligand of the tumor necrosis factor receptor family
RT that activates c-Jun N-terminal kinase in T cells.";
RL J. Biol. Chem. 272:25190-25194(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=BONE MARROW;
RX MEDLINE; 98227661.
RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA Boyle W.J.;
RT "Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT differentiation and activation.";
RL Cell 93:165-176(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=BONE MARROW STROMA;
RX MEDLINE; 98188248.
RA Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinoshita M.,
RA Mochizuki S.-H., Tomoyasu A., Yano K., Goto M., Murakami A., Tsuda E.,

RA Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda T.;
RT "Osteoclast differentiation factor is a ligand for
RT osteoprotegerin/osteoclastogenesis-inhibitory factor and is identical
RL to TRANCE/RANKL.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3597-3602(1998).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE-THYMIC LYMPHOMA;
RX MEDLINE; 98032977;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function.";
RL Nature 390:175-179(1997).
CC -!- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
CC AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL
CC PROLIFERATION.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
CC -!- TISSUE SPECIFICITY: HIGHER LEVELS IN THE BONE MARROW AND STROMAL
CC CELLS THAN SPLEEN, THYMUS AND LYMPH NODE.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
DR EMBL; AF053713; AAC40113.1; -.
DR EMBL; AF013170; AAC71061.1; -.
DR EMBL; AB008426; BAA25425.1; -.
DR EMBL; AF019048; AAB86812.1; -.
DR MGD; MGI:1100089; Tnfsf11.
DR INTERPRO; IPR000478; -.
DR PFAM; PF00229; TNF; 1.
DR PROSITE; PS00251; TNF_1; FALSE_NEG.
DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KW Signal-anchor.
FT DOMAIN 1 48 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 49 69 SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 70 316 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 99 99 G -> D (IN REF. 4).
SQ SEQUENCE 316 AA; 34944 MW; 08DF63A2BE00967A CRC64;

Query Match 100.0%; Score 1675; DB 11; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.5e-147;
Matches 316; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRRASRDYCKYLRSSEMGSGPGVPHGPHLPAPAPAPPAAASRSMFLALLGLGLGQ 60
Db 1 MRRASRDYCKYLRSSEMGSGPGVPHGPHLPAPAPAPPAAASRSMFLALLGLGLGQ 60

Qy 61 VVCSIALFLYFRAQMDPNRISEDSHCHFYRLRLHENAGLQDSTLESDTLPSDCRRMKQ 120
Db 61 VVCSIALFLYFRAQMDPNRISEDSHCHFYRLRLHENAGLQDSTLESDTLPSDCRRMKQ 120

Qy 121 AFOGAVQKELQIHVGQRFSGAPAMMEGSLDVAQRGKPEAQPFPAHLTINAASIPSGSHK 180
Db 121 AFOGAVQKELQIHVGQRFSGAPAMMEGSLDVAQRGKPEAQPFPAHLTINAASIPSGSHK 180

Qy 181 VTLSSWYHGRGWAKISNTLSNGKLRVNDGFYLYLANICFRHHETSGSVPTDYQLQMWY 240
Db 181 VTLSSWYHGRGWAKISNTLSNGKLRVNDGFYLYLANICFRHHETSGSVPTDYQLQMWY 240

Qy 241 VVKTSIKIPSSHNLMKGGSTKNWGSNFEHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
Db 241 VVKTSIKIPSSHNLMKGGSTKNWGSNFEHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300

Qy 301 DDATYFGAFKVDID 316
Db 301 DDATYFGAFKVDID 316

RESULT 2

Q9RLY0 Q9RLY0 PRELIMINARY; PRT; 313 AA.
ID Q9RLY0;
AC Q9RLY0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE OSTEOCLAST DIFFERENTIATION FACTOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RA Kodaira K., Kodaira K., Mizuno A., Yasuda H., Shima N., Murakami A.,
RA Ueda M., Higashio K.;
RT "Cloning and characterization of the gene encoding mouse osteoclast
RT differentiation factor.";
RL Gene 230:121-127(1999).
DR EMBL; AB022039; BAA36970.1; -.
DR EMBL; AB022036; BAA36970.1; JOINED.
DR EMBL; AB022037; BAA36970.1; JOINED.
DR EMBL; AB022038; BAA36970.1; JOINED.
DR INTERPRO; IPR000478; -.
DR PFAM; PF00229; TNF; 1.
DR PROSITE; PS00049; TNF_2; 1.
SQ SEQUENCE 313 AA; 34719 MW; 37D530B8BFC2842E CRC64;

Query Match 98.3%; Score 1646.5; DB 11; Length 313;
Best Local Similarity 99.1%; Pred. No. 6.4e-145;
Matches 313; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 MRRASRDYCKYLRSSEMGSGPGVPHGPHLPAPAPAPPAAASRSMFLALLGLGLGQ 60
Db 1 MRRASRDYCKYLRSSEMGSGPGVPHGPHLPAPAPAPPAAASRSMFLALLGLGLGQ 60

Qy 61 VVCSIALFLYFRAQMDPNRISEDSHCHFYRLRLHENAGLQDSTLESDTLPSDCRRMKQ 120
Db 61 VVCSIALFLYFRAQMDPNRISEDSHCHFYRLRLHENAGLQDSTLESDTLPSDCRRMKQ 120

Qy 121 AFOGAVQKELQIHVGQRFSGAPAMMEGSLDVAQRGKPEAQPFPAHLTINAASIPSGSHK 180
Db 121 AFOGAVQKELQIHVGQRFSGAPAMMEGSLDVAQRGKPEAQPFPAHLTINAASIPSGSHK 177

Qy 181 VTLSSWYHGRGWAKISNTLSNGKLRVNDGFYLYLANICFRHHETSGSVPTDYQLQMWY 240
Db 181 VTLSSWYHGRGWAKISNTLSNGKLRVNDGFYLYLANICFRHHETSGSVPTDYQLQMWY 237

Qy 241 VVKTSIKIPSSHNLMKGGSTKNWGSNFEHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 300
Db 238 VVKTSIKIPSSHNLMKGGSTKNWGSNFEHFYSINVGGFFKLRAGEEISIQVSNPSLLDP 297

Qy 301 DDATYFGAFKVDID 316
Db 298 DDATYFGAFKVDID 313

RESULT 3
O14788 O14788 PRELIMINARY; PRT; 317 AA.
AC O14788; O14723;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE TNF-RELATED ACTIVATION-INDUCED CYTOKINE (RANKL) (TRANSE) (OPGL)
DE (OSTEOPROTEGERIN LIGAND) (TUMOR NECROSIS FACTOR LIGAND).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BONE MARROW, AND PERIPHERAL BLOOD;

XX	MEDLINE; 98032977.
RA	Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA	Tometsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D.,
RA	Galibert L.;
RT	"A homologue of the TNF receptor and its ligand enhance T-cell growth
RT	and dendritic-cell function.;"
RL	Nature 390:175-179(1997).
RL	[2]
RN	SEQUENCE FROM N.A.
RP	TISSUE=LYMPH NODE;
RC	MEDLINE; 98227661.
RX	Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R.,
RA	Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H.,
RA	Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X.,
RA	Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J.,
RA	Boyle W.J.;
RT	"Osteoprotegerin ligand is a cytokine that regulates osteoclast
RT	differentiation and activation.;"
RL	Cell 93:165-176(1998).
RL	[3]
RP	SEQUENCE OF 73-317 FROM N.A.
RC	TISSUE=THYMOCYTES;
RX	MEDLINE; 97460112.
RA	Wong B.R., Rho J., Arron J., Robinson E., Orlickin J., Chao M.,
RA	Kalachikov S., Cayani E., Bartlett F.S. III, Frankel W.N., Lee S.Y.,
RA	Choi Y.;
RT	"FRANCE is a novel ligand of the tumor necrosis factor receptor family
RT	that activates C-Jun N-terminal kinase in T cells.;"
RL	J. Biol. Chem. 272:25190-25194(1997).
CC	-I- FUNCTION: OSTEOCLAST DIFFERENTIATION AND ACTIVATION FACTOR.
CC	AUGMENTS ABILITY OF DENDRITIC CELLS TO STIMULATE NAIVE T-CELL
CC	PROLIFERATION.
CC	-I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
CC	-I- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT
CC	WEAK IN SPLEEN, PERIPHERAL BLOOD LEUKOCYTES, BONE MARROW, HEART,
CC	PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.
CC	-I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
DR	EMBL; AF019047: AAB86811.1; -
DR	EMBL; AF053712: AAC39731.1; -
DR	EMBL; AF013171: AAC51762.1; -
DR	MIN: 602842; -
DR	INTERPRO; IPR000478; -
DR	PFAM; PF00229; TNF; 1.
DR	PROSITE; PS00251; TNF_1; FALSE_NEG.
DR	PROSITE; PS00049; TNF_2; 1.
KW	Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
KW	Signal-anchor.
FT	DOMAIN 1 47
FT	TRANSMEM 48 68
FT	DOMAIN 69 317
FT	CARBOHYD 171 171
FT	CARBOHYD 198 198
FT	CONFLICT 194 194
FT	SEQUENCE 317 AA; 35478 MW; 765176446348097F CRC64;
FT	CYTOPLASMIC (POTENTIAL).
FT	SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
FT	(POTENTIAL).
FT	EXTRACELLULAR (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	A -> G (IN REF. 3).

Query Match 84.6%; Score 1417.5; DB 4; Length 317;
Best Local Similarity 84.3%; Pred. No. 1.2e-123;
Matches 268; Conservative 16; Mismatches 31; Indels 3; Gaps 2;

[illegible]

QY	179	HKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYQLQM	239
DB	180	HKVTLSSWYHDRGWAKISNMTFSNGKLVNQDGFYYLYANICFRHHETSGDLATEYLQLM	239
QY	239	VYVYKTSIKTPSSHNLMKGGSTKNWGSNFBHFYSINVGGFFKLRAGEEISIQVSNPSLL	298
DB	240	VYVYKTSIKTPSSHTLMKGGSTKYWSNGBHFYSINVGGFFKLRAGEEISIEVSNPSLL	299
QY	299	DPDODATYFGAFKVQDID 316	
DB	300	DPDODATYFGAFKVRDID 317	
RESULT	4		
O97605		PRELIMINARY;	PRT; 260 AA.
ID	O97605		
AC	O97605;		
DT	01-MAY-1999 (TremBLrel. 10, Created)		
DT	01-MAY-1999 (TremBLrel. 10, Last sequence update)		
DT	01-MAY-2000 (TremBLrel. 13, Last annotation update)		
DE	CD40 LIGAND.		
GN	CD154.		
OS	Felis silvestris catus (Cat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RC	STRAIN=DOMESTICUS; TISSUE=THYMUS;		
RA	Hosie M.J., Willett B.J.;		
RT	"Adjuvant properties of feline CD154 (CD40 ligand).";		
RL	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF079105; AAD02954.1;		
DR	HSSP; P29965; ITALY.		
DR	INTERPRO; IPR000478;		
DR	PFAM; PF00229; TNF.1.		
DR	PROSITE; PS00251; TNF_1; 1.		
DR	PROSITE; PS00049; TNF_2; 1.		
SQ	SEQUENCE 260 AA; 28727 MW; 349FA0391FB7B932 CRC64;		
Query Match	9.88;	Score 164;	DB 6; Length 260;
Best Local Similarity	24.68;	Pred. No. 1.9e-07;	
Matches	71; Conservative	53; Mismatches 119; Indels	46; Gaps
QY	33	APSAAPAPPPAASRSFALALGILGQVVCSTALF-LYFRAOMDPNRISEDSTHCF--Y 89	
DB	9	APRSVAGCPP--VSMKTFMYLLVFLTQIGSALFAVYLHRRDK---IEDERNLYEDF 63	
QY	90	RILRLHENAGLDSTLESDTLDPDCRRMKQAFQGAQVOKELQHVGPQFSGAPAMMEGS 149	
DB	64	VFMKTLQCKNGEGALSIL-----NCEIKSRFE-AFLKEIMLNKTKKKNV----- 110	
QY	150	WLDVAQKGPAPQAFALHTTNAASIPSGSHKVTLSWYHDRGWAKISN--MTLSNGK-LR 206	
DB	111	---AMQKGDQDPVAAHV-ISEAS---SSTASVLOW-APKGYTTISSNLVLTLENGKQLA 161	
QY	207	VNODGFYYLYANICF-RHHETSGSVPTDYQLQWVYVVKTSIKTPSSH--LMKGGSTKN 263	
DB	162	VKROGLYYIAQVTFCSNRASQAP-----FIASLCIHPSPGSRVLRANAR--- 211	
QY	264	SGNSEFHYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312	
DB	212	SSSKPCGQSHLGGVFLHPGASVFVNVDTPQVSHGTGFTSFGLLKL 260	
RESULT	5		
O97626		PRELIMINARY;	PRT; 260 AA.
ID	O97626		
AC	O97626;		
DT	01-MAY-1999 (TremBLrel. 10, Created)		
DT	01-MAY-1999 (TremBLrel. 10, Last sequence update)		
DT	01-MAY-2000 (TremBLrel. 13, Last annotation update)		
DE	CD40 LIGAND.		


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GN CD40L.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RP SEQUENCE FROM N.A.
RA Hosie M.H., Willett B.J.;
RT "Adjuvant properties of canine CD40L.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF086711; AAD04375.1; -.
DR HSSP; P29965; 1ALY.
DR INTERPRO; IPR000478; -.
DR PFAM; PF00229; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 260 AA; 28688 MW; 604F69A19E98EB70 CRC64;

Query Match 9.2%; Score 154; DB 6; Length 260;
Best Local Similarity 24.7%; Pred. No. 1.6e-06;
Matches 72; Conservative 54; Mismatches 114; Indels 52; Gaps 17;

Qy 33 APSAPAPAPPPAASRSMELALGLGQVVCISALF-LYFRAQMDPNRISEDSHCF--Y 89
Db 9 ARSVATGPP--VSMKIFMYLLTVFLITQMIGSALFAVYLHRRLDK---IEDERNLYEDF 63
Qy 90 RLRLHENAGLDSTLESDTLDPDCRRMKQAFQAVOKELQHIIVGPORFSGAPAMMEGS 149
Db 64 VPMKTLQCNKGEGLSLL-----NCEIKSQFE-AFLKEIM-LNEMKKEENIAM---- 112
Qy 150 WLDVAQRGKPEAQPFALHTINAASIPSGSHKVTLSWYHRCWAKISN--MTLSNGK-LR 206
Db 113 -----QKGDQDPRIAAHVISEASSNPA-----SVLRW-APKGYITISNLVSLKNGKQLA 161
Qy 207 VNQDFYLYLANICF-RHETSGSVPTDYQLQMLVYVVKTSIKIPSSH--LMKGGSTKNW 263
Db 162 VKRQGLYVYAQVTCFSNRAASSQAP-----FVASICLHSPGTCSTERVLLRAASRGS 213
Qy 264 S---GNSEFHFYINVGGFKLRAGEEISIQVNSPSLLDPDQDATVFGAFKV 312
Db 214 SKPCGQQ-----SIHLGGVFELHPGASVFNVTDFSQVSHGFTGTSFGLLKL 260

RESULT 6
Q9TTJ3
ID Q9TTJ3 PRELIMINARY; PRT; 234 AA.
AC Q9TTJ3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE TUMOR NECROSIS FACTOR-ALPHA.
GN TNFA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
RN [1]
RP SEQUENCE FROM N.A.
RA Ishida N., Sato F., Hasegawa T.;
RT "Molecular cloning of equine tumor necrosis factor-alpha mRNA.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035735; BAA88349.1; -.
DR INTERPRO; IPR000478; -.
DR INTERPRO; IPR002959; -.
DR INTERPRO; IPR002960; -.
DR PFAM; PF00229; TNF; 1.
DR PROSITE; PR01234; TNECROSISFCT.
DR PRINTS; PR01235; TNFALPHA.
DR PRINTS; PR01236; TNFBETA.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 234 AA; 25430 MW; 2384D4950A21F377 CRC64;

Query Match 8.9%; Score 149; DB 6; Length 234;
Best Local Similarity 24.1%; Pred. No. 4.1e-06;
Matches 47; Conservative 38; Mismatches 72; Indels 38; Gaps 9;

Qy 133 IVGPORFSGAPAMMEGSWLDVAQRGK-----PEAQPFALHTINAASIPSGSHKVTLSWY 187
Db 55 VIGPQREEQLPNFAQ-SINLAQTLRSSRTPSPDKPAHVAVN-----PQAGQL---QWL 106
Qy 188 HDRGWAKISN-MTLSNGKLRVNDGFFYLYLANICFRHETSGSVPTDYQLQMLVYVVKTSI 246
Db 107 SGRANALLANGVKLTNDQLVVPDGLYLYISQVLFK-----GQGPCSTHVLTHHTISRLAV 162
Qy 247 KIPSSHNLKMG-----GSTKNWGSNSEFHFYINVGGFKLRAGEEISIQVSN 294
Db 163 SYPSKVNLLSAIKSLANTESPEQAEPW-----YEPIYLGGVFQLEKGDQLSAEINQ 215
Qy 295 PSLLD-PDQDATVFG 308
Db 216 PNYLDFAESGVYFG 230

RESULT 7
Q35853
ID Q35853 PRELIMINARY; PRT; 232 AA.
AC Q35853;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE TUMOR NECROSIS FACTOR ALPHA.
GN TNFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A/J;
RX MEDLINE; 97246744.
RA Iraqi F., Teale A.;
RT "Cloning and sequencing of the tnfa genes of three inbred mouse strains.";
RL Immunogenetics 45:459-461(1997).
DR EMBL; U68414; AAB65593.1; -.
DR HSSP; P01375; 4TSV.
DR INTERPRO; IPR000478; -.
DR INTERPRO; IPR002959; -.
DR PFAM; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRINTS; PR01235; TNFALPHA.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 232 AA; 25513 MW; 2ED6DA8E0DCAADD8 CRC64;

Query Match 8.8%; Score 148; DB 11; Length 232;
Best Local Similarity 24.6%; Pred. No. 5e-06;
Matches 48; Conservative 34; Mismatches 73; Indels 40; Gaps 9;

Qy 133 IVGPQR---FSGAPAMMEGSWLDVAQRGKPEAQPFALHTINAASIPSGSHKVTLS-SWYH 188
Db 55 VIGPQREKPNGLPLTSSMAQTLSSSQNSDKPAHVAVN-----HQVEQLEWLS 106
Qy 189 DRGWAKISN-MTLSNGKLRVNDGFFYLYLANICFRHETSGSVPTDYQLQMLVYVVK---- 243
Db 107 QRANALLANGMDLKNQVVPADGLYLVYISQVLFK-----GQGPCDYV-LLTHTVSREAI 160
Qy 244 -----TSIKPSSHNLKMGSTKNWGSNSEFHFYINVGGFKLRAGEEISIQVSN 294
Db 161 SYQEKVNLLSAVSPCKPTEGAELPW-----YEPIYLGGVFQLEKGDQLSAEYNL 213
Qy 295 PSLLD-PDQDATVFG 308
Db 214 PNYLDFAESGVYFG 228
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Db 160 VSYQTKVNLSSAIKSPCQRETPEGAKEPW-----YEPIYLGGVFQLEKGDRLSAEIN 212

Qy 294 NPSLLD-PDQDATYEG 308

Db 213 RPDYLDFAESGQVYEG 228

RESULT 12

O95150

ID O95150 PRELIMINARY; PRT; 174 AA.

AC O95150;

DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE VASCULAR ENDOTHELIAL CELL GROWTH INHIBITOR.

GN VEG1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-VASCULAR ENDOTHELIAL;

RA Yu G.-L., Zhai Y., Ni J., Iruela-Arispe L., Huang W.-Q., Xing L.,

RA Lu J., Kozak D., Jiang G.-W., Rojas L., Janat M.F., Buerger M.,

RA Gentz S., Lippman M.E., Aggarwal B.B., Ruben S., Gentz R., Li L.-Y.,

RA Yu G.-L.;

RT "A Novel Endothelial Cell-Specific Negative Regulator of

RT Angiogenesis.";

RT Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF039390; AAD08783.1; -.

DR HSSP; P01375; 1A8M.

DR INTERPRO; IPR000478; -.

DR PFAM; PF00229; TNF; 1.

DR PRINTS; PR01234; TNECROSISFCT.

DR PROSITE; PS50049; TNF_2; 1.

SQ SEQUENCE 174 AA; 20131 MW; CCB83BA7EE673B98 CRC64;

Query Match 8.4%; Score 140; DB 4; Length 174;

Best Local Similarity 28.3%; Pred. No. 1.9e-05;

Matches 39; Conservative 24; Mismatches 55; Indels 20; Gaps 5;

Qy 186 WYHDSGAKISN-WTLSNGKLVNDGGFYLYANICFRHH-----PTDYQLQM 238

Db 42 WEHELGLAFTKRMNMYTNKFLIPESGDYFIYQVTFRCMTSECSIRQAGRPKPDST 101

Qy 239 VYVVKTSIKIPSSHNLKMGST-----KNWSONSEFHYSINVGFFKLRAGEEISIQVS 293

Db 102 VYITKVDYSPEPTQLMGTSKVCVGSNW-----FQPIYLGAMFSLQEGDKLMVNV 154

Qy 294 NPSLLD-PDQDATYEGAF 310

Db 155 DISLVDTYTKEDKTFEGAF 172

RESULT 13

Q28320

ID Q28320 PRELIMINARY; PRT; 234 AA.

AC Q28320;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE TNF-ALPHA.

OS Capra hircus (Goat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Caprinae; Capra.

RN [1]

RP SEQUENCE FROM N.A.

RA Takakura H., Mori Y., Tatsumi M.;

RT "Molecular cloning of caprine TNF-alpha cDNA and its expression in

RT E.coli and insect cells.";

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; D86587; BAA13130.1; -.

DR HSSP; P01375; 4TSV.

DR INTERPRO; IPR000478; -.

DR INTERPRO; IPR002959; -.

DR PFAM; PF00229; TNF; 1.

DR PRINTS; PR01234; TNECROSISFCT.

DR PRINTS; PR01235; TNFALPHA.

DR PROSITE; PS00251; TNF_1; 1.

DR PROSITE; PS50049; TNF_2; 1.

SQ SEQUENCE 234 AA; 25519 MW; 9768E33BBABB041 CRC64;

Query Match 8.3%; Score 139; DB 6; Length 234;

Best Local Similarity 25.7%; Pred. No. 3.5e-05;

Matches 49; Conservative 30; Mismatches 82; Indels 30; Gaps 9;

Qy 133 IVGPQRFSGAPAMME-GSWLDVAQRKPEA---OPFAHLTINAASIPSGSHKVTLSWYH 188

Db 55 VIGPQREEQSPAGPSFNRPLVQTLRSSQASSNRPVAHVANI-----SAPQLRWGDSYA 110

Qy 189 DRGWAKISNMTLSNGKLVNQDGFYLYANICFRHH-----ETSGSVPTDYQLQM 238

Db 111 NA--LRANGVELKDNQLVWPTDGLYLIYSQVLFGRGHCPSPTPLTHTTISRIVSY-QTK 167

Qy 239 VYVVKTSIKIPSSHNLKMGSTKNWSONSEFHYSINVGFFKLRAGEEISIQVSNPSLL 298

Db 168 VNTL-SAIKSPCHRETPEGAKEPW-----YEPIYQGGVFQLEKGDRLSAEINQPEYL 219

Qy 299 D-PDQDATYEG 308

Db 220 DYAESGQVYEG 230

RESULT 14

O43557

ID O43557 PRELIMINARY; PRT; 240 AA.

AC O43557;

DT 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

DE TUMOR NECROSIS FACTOR SUPERFAMILY MEMBER LIGHT.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 98122340.

RA Mauri D.N., Ebner R., Montgomery R.I., Kochel K.D., Cheung T.C.,

RA Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.G.,

RA Ware C.F.;

RT "LIGHT, a new member of the TNF superfamily, and lymphotoxin alpha are

RT ligands for herpesvirus entry mediator.";

RL Immunity 8:21-30(1998).

DR EMBL; AF036581; AAC39563.1; -.

DR HSSP; P01375; 4TSV.

DR INTERPRO; IPR000478; -.

DR PFAM; PF00229; TNF; 1.

DR PROSITE; PS50049; TNF_2; 1.

SQ SEQUENCE 240 AA; 26351 MW; 49D0BF67E1390B39 CRC64;

Query Match 8.0%; Score 134.5; DB 4; Length 240;

Best Local Similarity 28.5%; Pred. No. 9.3e-05;

Matches 59; Conservative 30; Mismatches 85; Indels 33; Gaps 12;

Qy 121 AFGQVQKELQHVGPQ--RFSGAPAMMEGSLWDVAQ-RGKPEAQPFHAHLTINAASIPSG 177

Db 52 AVQGWFLQLLHWRIGEMVTRLPDGPA---GSWEQLQERRSHEVNPAAHLT-GANSSLTG 107

Qy 178 SHKVTLSWYHDSGAKISNMTLSNGKLVNQDGFYLYANICFRHHETSG-SVPTDYQLQ 236

Db 108 SGGPLL--WETQLGLAFLRGLSYHDGALVVTKAGYYIYSKV-----QLGGVGCPGLIAS 160

```

Qy 237 LMVY-VVKTSIKIPSSHLMKG-----GSKNWSGSEFHFYSINVGFFKLRAGE 286
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 161 TITHCLYKRTTRYPELELLVYQQSPCCGRATSSSRVW-WDSF-----LCGVVHLEAGE 213
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 287 EISQVSNPSLLD-PQDATYFGAFKV 312
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 214 EWVVRVLDRLVRLRDGTRSYFGAFMV 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
O18779
ID O18779 PRELIMINARY; PRT: 233 AA.
AC O18779;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE TUMOR NECROSIS FACTOR ALPHA.
GN TNFA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1].
RP SEQUENCE FROM N.A.
RC STRAIN=N'DAMA;
RA Iraqi F.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF011926; AAB84086.1; -.
DR HSP; P01375; 4TSV.
DR INTERPRO; IPR000478; -.
DR INTERPRO; IPR002959; -.
DR PFAM; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRINTS; PR01235; TNFALPHA.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS0049; TNF_2; 1.
SQ SEQUENCE 233 AA; 25395 MW; 8D8729025DE516B0 CRC64;

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Query Match      8.0%; Score 133.5; DB 6; Length 233;
Best Local Similarity 25.8%; Pred. No. 0.00011;
Matches 51; Conservative 30; Mismatches 72; Indels 45; Gaps 11;

Qy 133 IVGPQR--FSGAPAMMEGSLDVAQRKPEA---QPFAHLTINAASIPSGSHKVTLSWY 187
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 55 VIGQRESPGGPSI--NSPLVQTLRSSSQASSNKPVAHVAD-----INSPG 100
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 188 HDRGWAKISNMTLSNG-KLRVNO-----DGFYYLYANICFRHH-----ETSGSVP 231
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 101 QLRWWDSYANALMANGVKLEDNQLVVPADGLYLIYSQVLFERQGCPTPLFLTHITISRIA 160
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 232 TDYLQLMVYVVKTSIKIPSSHNLMMKGSTKWNWSGSEFHFYSINVGFFKLRAGEISIO 291
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 161 VSY-QTKVNIL-SAIKSPCHRETPWEAKPW-----YEFIYGGGVFQLEKGRLSAE 211
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 292 VSNPSSLDPQDATYFG 308
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 212 INLPDYLDYAESGGVYFG 229
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Search completed: December 29, 2000, 09:00:15
Job time: 48133 sec


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243: sThrSerIleLysIleProSerSerHisAsnLeuMetLysGlyGlySerT 260
467: ACCACGATCAGATCCCAAGTTCTCATACCTTGATGAAGGAGGAAGCA 418
260: hrLysAsnTrpSerGlyAsnSerGluPheHisPheTyrSerIleAsnVal 276
417: CTTAGTATTGGTCAGGAATATGATTCATTTTATTCATATAACGTT 368
277: GlyGlyPhePheLysLeuArgAlaGlyGluGluIleSerIleGlnValSe 293
367: GGTGGATTTTAAAGTTCGGTCTGGAGAGGAATCAGCATCGAGGTC 318
293: rAsnProSerLeuLeuAspProAspGlnAspAlaThrTyrPheGlyAlaP 310
317: CAACCCCTCTTACTTGATCCGATCCGATCAGGATGCAACATACTTTGGGCT 268
310: heLysValGlnAspIleAsp 316
267: TTAAGTTCGAGATATAGAT 248

seq_name: gb_gss12:AQ827168

seq_documentation_block:
LOCUS AQ827168 529 bp DNA GSS 27-AUG-1999
DEFINITION HS_5256_B2_G09_77A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=832 Col=18 Row=N, DNA sequence.
ACCESSION AQ827168
VERSION AQ827168.1 GI:5793230
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 529)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 832 row: N column: 18
Seq primer: T7
Class: BAC ends
High quality sequence stop: 529.
location/Qualifiers
1..529
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=832 Col=18 Row=N"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
/note="vector: pBACE3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACE3.6 vector at EcoRI sites"
147 a 121 c 102 g 153 t

BASE COUNT
ORIGIN

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alignment_scores:

Quality: 315.50 Length: 82
Ratio: 4.264 Gaps: 1
Percent Similarity: 90.244 Percent Identity: 78.049

alignment_block:

US-08-989-362-2 x AQ827168/rev ..

Align seg 1/1 to reverse of: AQ827168 from: 1 to: 529

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235 LeuGlnLeuMetValTyrValValLysThrSerIleLysLeuProSerSe 251
|||||
501 CTTCAACTAATGGTGTGTCACCTA...NACCAGCATCAAAATCGCAAGTTC 455
|||||
251 rHisAsnLeuMetLysGlySerThrLysAsnTrpSerGlyAsnSerG 268
|||||
454 TCATACNTGATGAAGGAGCAGCACCAAGTATTGGTCAGGGAATTCGT 405
|||||
268 luPheHisPheTyrSerIleAsnValGlyGlyPhePheLysLeuArgAla 284
|||||
404 AATTCCATTTTATTCATAAACGTTGGTGCATTTTCTAAGTTACGGTCT 355
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285 GlyGluGluLysSerIleGlnValSerAsnProSerLeuLeuAspProAs 301
|||||
354 GGAGAGGAATCAGCATCGAGGTCTCCAAAGCCCTCTTACTGGATCCGGA 305
|||||
301 pGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspIleAsp 316
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304 TCAGGATGCAACATACCTTTGGGGCTTTTAAAGTTCGAGATATAGAT 259
|||||

```

seq_name: gb_est33:BE042463

seq_documentation_block:

LOCUS BE042463 618 bp mRNA EST 08-JUN-2000
DEFINITION ho22c06.x1 NCI-CGAP_Col14 Homo sapiens cDNA clone IMAGE:3038122 3'
similar to SW-TRAI- HUMAN P50591 TNF-RELATED APOPTOSIS INDUCING
LIGAND ;, mRNA sequence.
ACCESSION BE042463
VERSION BE042463.1 GI:8359516
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 618)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 421.
location/Qualifiers
1..618
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/db_xref="taxon:9606"
/clone="IMAGE:3038122"
/clone_lib="NCI-CGAP_Col14"
/tissue_type="moderately-differentiated adenocarcinoma"
/lab_host="DH10B"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.

FEATURES

source


```

LOCUS      AW945165      718 bp      mRNA      EST      31-MAY-2000
DEFINITION EST361358 MAGE resequencences, MAGA Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW945165
VERSION    AW945165.1  GI:8122916
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 718)
AUTHORS    Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
            J.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
            Quackenbush,J.
TITLE      Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
JOURNAL    Unpublished (2000)
COMMENT    Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johnq@tigr.org
            Plate: 0
            Seq primer: Reverse.
            Location/Qualifiers
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_lib="MAGE resequencences, MAGA"
                /note="Vector: pluescriptskm"
BASE COUNT 271 a 136 c 130 g 179 t 2 others
ORIGIN

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US-08-989-362-2 x AW945165      ..
Align seg 1/1 to: AW945165      from: 1 to: 718
183 LeuSerSerTrpTyrHisAspArg...GlyTrpAlaLysIleSerAsnMe 198
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12 ATAACCTCTGGGAATCATCAAGAGTGGCATTCATCTCTGAGCAACTT 61
198 tThrLeuSerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTrL 215
   : ||| |||||::||| ::::: ||| ::::: ||| |||||::|||
62 GCATTGTAGGAATGGTGAAGTGGTATCCATCCATGAAAAAGGTTTACTACA 111
215 euTyrAlaAsnIleCysPheArgHisGluThrSerGlySerValPro 231
   ::||::: ||::: ||||| ::||| ::|||
112 TCTATTCCAACATACACTTCTCCATTCAGGAGGAAATAAAGAAACACA 161
232 ThrAspTyrLeuGlnMetValTyrValValLysThrSerIleLysI 248
   ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
162 AGAACGACAACAATAGTCTCAATATATTACAAATACACA...AGTTA 208
248 eProSerSerHisAsnLeuMetLysGlyGlySerThrLysAsnTrpSerG 265
   ||::: |||||::||| ::||| ::||| ::||| ::||| ::|||
209 TCCTGACCCATATATTCTTCAATGAAAGTCTAGAAATAGTTGTGCTCA 258
265 lyAsnSerGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLys 281
   ::::: ||::: ||::: ||||| ::||| ::||| ::||| ::|||
259 AGATGTCAGAAATAGACACTCTATTCCATCTATCAAGGGGGAATATTGAG 308
282 LeuArgAlaGlyGluGluIleSerIleGlnValSerAsnProSerLeuLe 298
   ||::: ||::: ||::: ||::: ||::: ||::: ||::: ||:::
309 CTTAGGAAAATGACAGAAATTTTGTCTGTGAACAAATGACCACTTGAT 358
298 uAspProAspGlnAspAlaThrTyrPheGlyAlaPheLysVal 312

```

```

::||| |||::: |||::: |||::: |||::: |||::: |||::: |||
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seq_documentation_block:
LOCUS      AQ817650      413 bp      DNA      GSS      26-AUG-1999
DEFINITION HS_52653_B1_D03_SpeE RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=841 Col=5 Row=H, DNA sequence.
ACCESSION  AQ817650
VERSION    AQ817650.1  GI:5780043
KEYWORDS   GSS.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 413)
AUTHORS    Mahairas,G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
TITLE      Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
JOURNAL    Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
MEDLINE    99380589
COMMENT    Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 841 row: H column: 5
            Seq primer: SP6
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            High quality sequence stop: 413.
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                /clone_lib="RPCI-11 Human Male BAC Library"
                /sex="male"
                /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                Male blood DNA was isolated from one randomly chosen donor
                and partially digested with a combination of EcoRI and
                EcoRI Methylase. Size selected DNA was cloned into the
                pBACe3.6 vector at EcoRI sites"
BASE COUNT 108 a 82 c 100 g 123 t
ORIGIN

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US-08-989-362-2 x AQ817650      ..
Align seg 1/1 to: AQ817650      from: 1 to: 413
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5 TCTGAATTCATTTTATTCATTAACGTTGGCGGATATTTAAGTTACG 54
283 gAlaGlyGluGluIleSerIleGlnValSerAsnProSerLeuLeuAspP 300
   ::::: ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

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55 GTCTGGAGGAAATCATCGAGGCTCTCCAACCCCTCTTACTGGATC 104
300 roAspGlnAspAlaThrTyrPheGlyAlaPheLysValGlnAspIleasp 316
105 CCGATCAAGATGCAACATCTTTGGGGCTCTTAAGAGCGAGATATGGAT 154
seq_name: gb_est20:AW104819
seq_documentation_block:
  LOCUS AW104819 585 bp mRNA EST 20-OCT-1999
  DEFINITION xs7b10.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2597851 3'
  similar to SW:TRAI_HUMAN P50591 TNF-RELATED APOPTOSIS INDUCING
  LIGAND 1, mRNA sequence.
  ACCESSION AW104819
  VERSION AW104819.1 GI:6075554
  KEYWORDS EST.
  SOURCE human.
  ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 585)
  REFERENCE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  TITLE Tumor Gene Index
  JOURNAL Unpublished (1997)
  COMMENT Contact: Robert Strausberg, Ph.D.
  Tel: (301) 496-1550
  Email: Robert.Strausberg@nih.gov
  Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
  Emmert-Buck, M.D., Ph.D.
  cDNA Library Preparation: Life Technologies, Inc.
  cDNA Library Arrayed by: Greg Lennon, Ph.D.
  DNA sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  www-bio.llnl.gov/bbrp/image/image.html
  Seq primer: -400P from Gibco
  High quality sequence stop: 405.
  FEATURES
  source
    1..585
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone_lib="IMAGE:2597851"
    /clone_lib="NCI_CGAP_Ov23"
    /tissue_type="tumor, 5 pooled (see description)"
    /lab_host="DH10B"
    /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI;
    Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
    Average insert size 1.35 kb. Tumor types include: mixed
    Mullerian tumor, papillary serous, clear cell, spindle
    cell. All are primary tumors, metastasis positive. Life
    Technologies catalog #: 11534-013"
  BASE COUNT 146 a 111 c 105 g 221 t 2 others
  ORIGIN

alignment_scores:
  Quality: 206.00 Length: 132
  Ratio: 2.264 Gaps: 3
  Percent Similarity: 68.939 Percent Identity: 35.606

alignment_block:
US-08-989-362-2 x AW104819/rev ..
Align seg 1/1 to reverse of: AW104819 from: 1 to: 585
183 LeuSerSerTrpTyrHisAspArg...GlyTrpAlaLysIleSerAsnMe 198
552 ATAACCTNTGGTCAATCAAGAGTGGGATTCATCTCCCGAGCAACTT 503
198 tThrLeuSerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTrL 215
: ||| |||||:||||| :|||:|||||:|||||:
502 GCACCTTGAGGAATGGTGAAGTGGTCATCCATCCGAAAGGGTTTACTACA 453
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215 euTyrAlaAsnIleCysPheArgHisGluThrSerGlySerValPro 231
:|||||:||||| :|||:|||||
452 TCATTATCCCAACATACATCTTCGATTTCCAGGAGAAATAAAGAAACACA 403
232 ThrAspTyrLeuGlnLeuMetValTyrValValLysThrSerIleLysI 248
:~: |||||:||||| :|||:|||||
402 AAGAAGCAGACAACAATGGTCCAATATATTACAAATACACA...AGTTA 356
248 eProSerSerHisAsnLeuMetLysGlySerThrLysAsnTrpSerG 265
|||||: |||||:||||| :|||:|||||
355 TCCTGACCCCTATATGTTGATGAAAGTCTAGAAATAGTTGTTGGTCTA 306
265 lyAsnSerGluPheHisPheTyrSerIleAsnValGlyGlyPhePhe 281
:|||||:||||| :|||:|||||
305 AAGATGAGAATATGGACTCTATTCATCTATCAAGGGGGAATATTGAG 256
282 LeuArgAlaGlyGluGlnIleSerIleGlnValSerAsnProSerLeu 298
:|||||:||||| :|||:|||||
255 CTTAAGGAAATGACGAATTTTGTCTCTAACAATGAGCACTTGAT 206
298 uAspProAspGlnAspAlaThr.TyrPheGlyAlaPheLysVal 312
:|||||:||||| :|||:|||||
205 AGACATGGACCATGACAGCAGTCTTTTCGGGGCCTTTTGTAGTT 162
seq_name: gb_est32:BE005955
seq_documentation_block:
  LOCUS BE005955 604 bp mRNA EST 05-JUN-2000
  DEFINITION RCO-BN0121-210300-031-e03 BN0121 Homo sapiens cDNA, mRNA sequence.
  ACCESSION BE005955
  VERSION BE005955.1 GI:8266188
  KEYWORDS EST.
  SOURCE human.
  ORGANISM Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 604)
  REFERENCE Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
  Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
  Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
  Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
  M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
  Simpson,A.J.
  TITLE Shotgun sequencing of the human transcriptome with ORF expressed
  sequence tags
  JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE 20202663
  COMMENT Contact: Simpson A.J.G.
  Laboratory of Cancer Genetics
  Ludwig Institute for Cancer Research
  Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
  Brazil
  Tel: +55-11-2704922
  Fax: +55-11-2707001
  Email: asimpson@ludwig.org.br
  This sequence was derived from the FAPESP/LICR Human Cancer Genome
  Project. This entry can be seen in the following URL
  (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=et2=RC0-BN0121-210
  300-031-e03&t3=2000-03-21&t4=1)
  Seq primer: puc 18 forward
  High quality sequence start: 29
  High quality sequence stop: 164.
  Location/Qualifiers
    1..604
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone_lib="BN0121"
    /dev_stage="Adult"
    /note="Organ: breast_normal; Vector: puc18; Site_1: SmaI;
    Site_2: SmaI; A mini-library was made by cloning products
    derived from ORESTES PCR (U.S. Letters Patent application
    No. 196,716 - Ludwig Institute for Cancer Research)
```


DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbr/image/image.html

Possible reversed clone: polyT not found
Seq primer: -40UP from Gibco
High quality sequence stop: 383.

FEATURES

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1. 502
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2680705"
/clone_lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"

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/rad_noscl- D110B
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.72 kb. Life Technologies catalog #:

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BASE COUNT	129 a	93 c	87 g	193 t
ORIGIN				

alignment_scores:		
Quality:	155.00	Length: 123
Ratio:	1.987	Gaps: 4
Percent Similarity:	63.415	Percent Identity: 35.772

alignment_block: US-08-989-362-2 x AW191932/rev

Align seg 1/1 to reverse of: AW191932 from: 1 to: 502

200. LeuSerAsnGlyLysLeuArgValAsnClnAspGlyPheTyrTyLeuTy 216

 496. TTGAGGAATCGTGAACATGGTCATCCATGAAAGGGTT.TACTACATCTA 448

 216 rAlaAsnIleCysPheArgHisGlu. 225

 447. TTCCCAACATACCTTCGATTTTCAGGAGGAATAAAGAAACCAAGAC 398

226ThrSerGlySerValProThrAspTyrLeuGlnLeu..MetValTy	240
	:::	
397	[GACAAACAATGGGCCAATA.....TAITTTTCAATTACACAGGTGA	357
	:::	
240	rvalValLysThrSerIleLysPheProSerHisAsnLeuMetLysG	257
	:::	
356	T.....CCTGACCCCATATGTGTGATGAAAA	331

273
257 lvGlySerThrLysAsnTrpSerGlyAsnSerGluPheHisSer 273
::: : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
330 GTCTAGAAATATTGTGGTCTAAGAATGCAGAAATGGCATTTATCC 281

274 IleAsnValGlyGlyPhePheLysLeuArgAlaGlyGluGluIleSerIle 290
||| ||||| ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
280 ATCTATCAGCGGGGAATTTTGACCTTAAGAAAATGACAGAAATTTTGT 231

290 eGlnValSerAsnProSerLeuLeuAspProCaspGlnAspAlaThrTyrP 307
 .|.|||||.....
 230..TTCTGTAAACAAYAGCACCTTGATAGACATGGACCATGAAGCCAGTTTT 181

307 heGlyAlaPheLysVal 312
 ..|||.....
 180 TTGGGGCGCTTTTAGTT 164

seq_name: gb_est8:AI095853

seq_documentation_block:	468 bp	mRNA	EST	05-OCT-1998
LOCUS	AI095853			
DEFINITION	qB26d04.x1 Soares_pregnant_uterus_NBHPU Homo sapiens cDNA clone IMAGE:1697383 ; similar to SW:TRAI_HUMAN P50591 TNF-RELATED			
		APOTOPSIS INDUCING LIGAND ;		
		RNA sequence.		

ACCESSION AT095853
VERSION AT095853.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE AUTHORS TITLE	JOURNAL COMMENT
<p>1. <i>Journal of the American Medical Association</i>, 1964, 191: 1000-1001.</p> <p>2. <i>Journal of the American Medical Association</i>, 1964, 191: 1000-1001.</p>	<p>1. <i>Journal of the American Medical Association</i>, 1964, 191: 1000-1001.</p> <p>2. <i>Journal of the American Medical Association</i>, 1964, 191: 1000-1001.</p>

Email: Robert.Strausberg@nih.gov
 This clone is available royalty-free through LNL ; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 1113 Std Error: 0.00
 Seq primer: -40ml3 fwd. Et from Amersham
 High quality sequence stop: 390

[illegible]

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location/Vuallilicis
1. .468
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/db_xref="taxon:9606"
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/clone_lib="Soares_pregnant_uterus_NbHPU"
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/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
AATGGAAGAAATTCGGCGCGCCCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by M. Estiva Bocardo."

```

BASE COUNT	118 a	81 c	81 g	188 t
ORIGIN				

. alignment scores:

Quality:	153.50	Length:	100
Ratio:	2.132	Gaps:	3
Percent Similarity:	72.000	Percent Identity:	36.000

alignment block:

US-08-989-362-2 x AI095853/rev

Align seq 1/1 to reverse of: AI095853 from: 1 to: 468

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214 TyrLeuTyrAlaAsnIleCysPheArg...HisIisGluThrSerGlySe 229
      ::::||||:||||| ::::||||:||||| ::::||||:||||| ::::
468 TAGATCTATTGCCAACATACTTTTCGATTGCAGGAGGAAATAAAAGAGA 419
      ::::||||:||||| ::::||||:||||| ::::||||:||||| ::::
229 rValProThrAspTyrLeuGlnLeuMetValTyrValValLysThrSerI 246
      ::::||||| :|||:||||:||||:||||:||||| :|||:||||:
418 CACAAAGACCGAC...AAACAATGGTCCATATATTTACAATAACACA. 373
      ::::||||:||||| :|||:||||:||||:||||:||||| :|||:
246 lelysIleProSerSerHisAsnLeuMetLysGlyGlySerThrLysAsn 262
      ::::||||:||||| :|||:||||:||||:||||:||||| :|||:
372 .AGTTATCTCTGACCCCTATATTGTGTGATGAAGAAGTCTAGAAATAGTTGT 325
      ::::||||:||||| :|||:||||:||||:||||:||||| :|||:
263 TrpSerGlyAsnSerGluPheHisPheTyrSerIleAsnValGlyGlyPh 279
      :|||:||||:||||| :|||:||||:||||:||||:||||| :|||:
324 TGGTCTCAAGATGCAGAAATATGGACTCTATCCATCTATCAAGGAGGAA 275
      :|||:||||:||||| :|||:||||:||||:||||:||||| :|||:
279 ePheLysLeuArAlaGlyGluGluIleSerIleGlnValSerAsnProS 296
      :|||:||||:||||| :|||:||||:||||:||||:||||| :|||:
274 ATTTAGCTTTAAGGAAATGACAGAAATTTTGTCTTCTGTACCAATAGC 225
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296 erLeuLeuAspProAspGlnAspAlaThrTyrPheGluValaPheLysVal 312

```

```

|||||
224 ACTGATAGACATGACCATGAAGCCAGTTTTCGGGGCCTTTTACTT 175
|||||

```

seq_name: gb_est3:AA298009

seq_documentation_block: 320 bp mRNA EST 18-APR-1997
 LOCUS AA298009
 DEFINITION EST113646 T-cell lymphoma Homo sapiens cDNA 5' end similar to Apo-2
 Ligand (tumor necrosis factor), mRNA sequence.

ACCESSION AA298009
 VERSION AA298009.1 GI:1950414
 KEYWORDS EST.
 SOURCE human.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS
 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
 ,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
 ,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
 Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
 ,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,
 Gnelm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,
 Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
 Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
 Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
 Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.,
 Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
 Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,
 Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon
 ,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
 Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

96026280

COMMENT

Other_ESTS: THCL83094
 Contact: Kerlavage, AR
 Bioinformatics

The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056

Fax: 3018699423
 Email: arkerlav@tigr.org

For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/cdb/hgl/hgl1.html>)
 Seq primer: M13 Reverse.

FEATURES

Location/Qualifiers
 1..320
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 /db_xref="ATCC (inhost):165358"
 /db_xref="taxon:9606"
 /clone_lib="T-cell lymphoma"
 /cell_type="T-lymphocyte"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI"

BASE COUNT 114 a 56 c 65 g 84 t 1 others
 ORIGIN

alignment_scores:

Quality: 153.00 Length: 102
 Ratio: 2.250 Gaps: 2
 Percent similarity: 66.667 Percent Identity: 34.314

alignment_block:

US-08-989-362-2 x AA298009 ..

Align seg 1/1 to: AA298009 from: 1 to: 320

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183 LeuSerSerTrpTyrHisAspArg...GlyTrpAlaLysIleSerAsnMe 198
:|||||
13 ATAAACTCTCTGGGAATCATCAAGAGTGGGCATTCATCTCTGAGCAACTT 62
:|||||
198 tThrLeuSerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrTrpL 215
:|||||
63 GCACITGAGGAATGGTGAACATGCTCATCCATGAAAAGGCTTTACTACA 112
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215 euTyrAlaAsnIleCysPheArgHisHisGlyThrSerGlySerValPro 231
:|||||
113 TCTATTCTCCAAACATACCTTTTCGATTTCAGGAGGAAATAAAGAAACACA 162
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232 ThrAspTyrLeuGlnLeuMetValTyrValValLysThrSerIleLysII 248
:|||||
163 ACAGACGACAGCAAAATGTCCTCAATATATTNCAATATACACA...AGTTA 209
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248 eProSerSerHisAsnLeuMetLysGlyGlySerThrLysAsnTyrSerG 265
:|||||
210 TCTTGACCTTATATTGTTGATGAAAAGTGTAGAAATAGTTGTGGCTCA 259
:|||||
265 lyAsnSerGluPheHisPheTyrSerIleAsnValGlyGlyPhePheLys 281
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260 AAGATGCAGCAATATGGACTCTATTCCATCTATCAAGGGGATATTTGAGC 309
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282 LeuArg 283
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310 TTAAGG 315

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seq_name: gb_est11:AI626285

seq_documentation_block: 218 bp mRNA EST 23-APR-1999

LOCUS AI626285

DEFINITION fc12f06.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to
 SW:TRAI_MOUSE P50592 TNF-RELATED APOPTOSIS INDUCING LIGAND ;, mRNA
 sequence.

ACCESSION AI626285

VERSION AI626285.1 GI:4663085

KEYWORDS EST.

SOURCE zebrafish.

ORGANISM Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Rasbora; Danio.

REFERENCE

1 (bases 1 to 218)

AUTHORS

Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
 ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
 ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
 Waller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
 Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
 and Wilson,R.

WashU Zebrafish EST Project 1998

Unpublished (1998)

Contact: Stephen L. Johnson

Washington University School of Medicine

444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: zbrafish@watson.wustl.edu

cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
 Matthew Clark. DNA Sequencing by: Washington University Genome
 Sequencing Center Clone Distribution: Genome Systems, St. Louis,
 Missouri (web address: www.genomesystems.com) (email contact:
 info@genomesystems.com) and Research Genetics, Huntsville, Alabama
 (web address: www.resgen.com) (email contact: info@resgen.com) and
 Ressourcenzentrum Primatendatenbank, Berlin, Germany (web address:
www.rzp.de)

Possible reversed clone: similarity on wrong strand

Seq primer: T3 ET from Amersham

High quality sequence stop: 113.

FEATURES

source

1..218
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 /db_xref="taxon:7955"


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398 GTATGACAGCCCTGCTGGCAAGTCAAGTGGCCACTCCGTCAGCTCGTT 349
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127 GlnLysGluLeuGlnHisIleValGlyProGlnArgPheSerGlyAlaPr 143
    :|||::  ::  |||  |||
348 AGAAAGAAAAGCAACAAATATTCTCCCTA..... 317
143 oAlaMetMetGluGlySerTrpLeuAspValAlaGlnArgGlyLysProG 160
    |||  ::|||  ;
316 .....GTGAGAGAAAGAGGTCTCTCAGA 295
160 luAlaGlnProPheAlaHisLeuThr.....IleAsnAla 171
    ::::  |||||::|  |||::
294 GAGTAGCA.....GCTCACAATACTGGGACCAGGAGGAAGCAACACA 251
172 AlaSerIleProSerGlySerHisLysValThrLeu.....Se 184
    |||  |||:::  ::|  ::|
250 TTGTCCTTCCAACTCCAAGATGAAAGGCTCTGGGCCCAAAATAA 201
184 rSerTrpTyrrHisAspArg...GlyTrpAlaLysIleSerAsnMetThrL 200
    :|||  ::|  |||  ::  ::|||  ::|
200 CTCCTGGGAATCATCAAGGAGTGGGCATTTCCTGAGCAACTTGCACT 151
200 euSerAsnGlyLysLeuArgValAsnGlnAspGlyPheTyrrTyrrLeuTyr 216
    ||  |||||  ::|  :::::  |||||  ::|  ::|
150 TGAGGAATGGTGAAGTGGTCAATGAAAGGGTTTACTACATCTAT 101
217 AlaAsnIleCysPheArgHisHisGlu 225
    ::::  |||||  ::|
100 TCCGATACATACATTTCGATTTCAGGAG 74
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